

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 3 MRAPAOIFGILLFPGTRCDIOMTQSPSSLSASIGERVSLTCRASODIGSLNMLQOEP 62
 1 MGAPAOILGILLFPGTRCDIOMTQSPSSLSASIGRVSLTCRASODIGINLHMLQOEP 60

Qy 63 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVYICLOYASSPFTGG 122
 61 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVAYYCLOYASSPFTGG 120

Db 123 GTKLEIKR 130
 121 GTKLEIKR 128

Qy 121 GTKLEIKR 128

RESULT 2
 ID KV5H MOUSE STANDARD; PRT; 117 AA.
 P01641:
 21-JUL-1986 (REL. 01, CREATED)
 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81064681.
 RA MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
 RL CELL 21:793-799(1980).
 DR EMBL; X00880; G197444; -.
 DR PIR; A01924; KVM53B.
 DR HSSP; P01607; 1EGV.
 DR IMMUNOGLOBULIN V REGION; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 22 IG KAPPA CHAIN V-V REGION (MOPC 173B).
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 12954 MW; 38F2B08C CRC32;

Query Match
 Best Local Similarity 80.0%; Pred. No. 1.09e-125;
 Matches 92; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Db 3 MRAPAOIFGILLFPGTRCDIOMTQSPSSLSASIGERVSLTCRASODIGINLHMLQOEP 62
 1 MGAPAOILGILLFPGTRCDIOMTQSPSSLSASIGRVSLTCRASODIGINLHMLQOEP 60

Qy 63 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVYICLOYASSP 117
 61 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVAYYCLOYASSP 115

Db 61 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVAYYCLOYASSP 115

RESULT 3
 ID KV5H MOUSE STANDARD; PRT; 128 AA.
 P01637:
 21-JUL-1986 (REL. 01, CREATED)
 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81052342.
 RA ALTENBURGER W., STEINMETZ M., ZACHAU H.G.;

RL NATURE 287:603-607(1980).
 DR EMBL; V00772; G762979; -.
 DR PIR; A01920; KVM5TL.
 DR HSSP; P01607; 11IF.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION (T1).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 127 FRAMEWORK 4.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SO SEQUENCE 128 AA; 14385 MW; 87009E44 CRC32;

Query Match
 Best Local Similarity 57.0%; Score 581; DB 1; Length 128;
 Matches 81; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Db 1 MRPAOIFGILLFPGTRCDIOMTQSPSSLSASIGERVSLTCRASODIGINLHMLQOEP 60
 1 MGAPAOILGILLFPGTRCDIOMTQSPSSLSASIGRVSLTCRASODIGINLHMLQOEP 60

Qy 61 GKSPTLLYRANLVDGVPKRFSGSGSDYSLTISLESEDFVYICLOYDEPPLFGA 120
 61 DGTIKRLIYATSSLDGVPKRFSGSGSDYSLTISLESEDFVAYYCLOYASSPFTGG 120

Db 121 GTKLEIKR 128
 121 GTKLEIKR 128

Qy 121 GTKLEIKR 128

RESULT 4
 ID KV1H HUMAN STANDARD; PRT; 129 AA.
 P04431:
 13-AUG-1987 (REL. 05, CREATED)
 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85014148.
 RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
 DR EMBL; X00965; G296684; ALT_TERM.
 DR PIR; A01883; K1H0WK.
 DR HSSP; P01607; 2EGW.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 22 IG KAPPA CHAIN V-I REGION (WALKER).
 FT CHAIN 23 129 FRAMEWORK 1.
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SO SEQUENCE 129 AA; 14069 MW; 99925172 CRC32;

Query Match
 Best Local Similarity 54.8%; Score 558; DB 1; Length 129;
 Matches 82; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Db 3 MRPAOILGILLFPGTRCDIOMTQSPSSLSASIGRVSLTCRASODIGINLHMLQOEP 62
 1 MGAPAOILGILLFPGTRCDIOMTQSPSSLSASIGRVSLTCRASODIGINLHMLQOEP 60


```

QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSASIGRVSLTCRASODIGINLHWLQOE 60
Db 63 GKAPLLIYAASLSQSGVTSRFGSGSGCTDFTLTISLQPEDSATYYCOQSYTLITFGQ 122
QY 61 DGTIKRLIYATSSLSGSGVPRKFRSGSRGSDYSLTISLSEBDFVAYYCLQYASSPTFFGG 120
Db 123 GTRLEIK 129
QY 121 GTRLEIK 127

RESULT 5
ID KVL1_HUMAN STANDARD: PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK101) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
SEQUENCE FROM N.A.
RA MEDLINE; 81098966.
RA BENTLEY D.L.; RABBITTS T.H.;
RA NATURE 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83129397.
RX BENTLEY D.L.; RABBITTS T.H.;
RL CELL 32:181-189(1983).
DR EMBL; J00244; G185970; -
DR EMBL; K01324; G185994; -
DR EMBL; Y00558; G33177; -
DR PIR; A01881; K1H011.
DR PIR; A21056; A21056.
DR HSSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION (HK101).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA; 12799 MW; B02D3EAL CRC32;

Query Match
Best Local Similarity 53.48; Score 544; DB 1; Length 117;
Matches 77; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Db 3 MRVPAOLIGLLLCFPGARCDIOMTOSPSLSASVGDRTVITTCRARGSSMLAWQOKR 62
QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSLSLGRVSLTCRASODIGINLHWLQOE 60
Db 63 GKAPLLIYAASLSQSGVTSRFGSGSGCTDFTLTISLQPEDSATYYCOQSYTLITFGQ 117
QY 61 DGTIKRLIYATSSLSGSGVPRKFRSGSRGSDYSLTISLSEBDFVAYYCLQYASSPTFFGG 115

RESULT 6
ID KVL1_HUMAN STANDARD: PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (DAUDI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

```

```

OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85014148.
RA KLOBECK H.G.; COMBIANO G.; ZACHAU H.G.;
RL NUCLEIC ACIDS RES 12:6995-7006(1984).
DR EMBL; K02134; G185822; -
DR EMBL; X00966; G296685; ALT_TERM.
DR PIR; A01884; K1H011.
DR HSSP; P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129
FT SEQUENCE 129 AA; 14235 MW; 05B40B5E CRC32;

Query Match
Best Local Similarity 52.98; Score 539; DB 1; Length 129;
Matches 75; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

Db 3 MRVPAOLIGLLMLRVRCDIOMTOSPSLSASVGDRTVITTCRAGHNTNFTSWQOKR 62
QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSLSLGRVSLTCRASODIGINLHWLQOE 60
Db 63 GKAPLLIYAASLSQSGVTSRFGSGSGCTDFTLTISLQPEDSATYYCOQSYTLITFGQ 122
QY 61 DGTIKRLIYATSSLSGSGVPRKFRSGSRGSDYSLTISLSEBDFVAYYCLQYASSPTFFGG 120
Db 123 GTRVNDK 129
QY 121 GTRLEIK 127

RESULT 7
ID KVL1_MOUSE STANDARD: PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (MOPC 173).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76091934.
RA SCHIFF C.; FOUGEREAU M.;
RL EUR. J. BIOCHEM. 59:525-537(1975).
CC - THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01926; KVM573.
DR HSSP; P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION.
FT SIGNAL 1 23
FT CHAIN 24 108 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DOMAIN 98 108 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
FT SEQUENCE 108 AA; 11819 MW; EA186054 CRC32;

Query Match
Best Local Similarity 52.78; Score 537; DB 1; Length 108;
Matches 69; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

```

```

Matches 5: Conservative 16: Mismatches 17: Indels 0: Gaps 0:

Db 1 D10MT0TSSLSASL6GRVAT1SCASG0S1GN1YLBMY0QRKDGIVKLLIYTSLSHSVPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 21 D10MT0SPSSLSASL6GRVAT1SCASG0D1GIN1HML0Q0EPDGT1KRLIYATSSLSGCVPK 80
1 RFSGSGCTEFTLTINSLOPEDFATYYCLOYSSFPWTGFGCTKVEVKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 81 RFSGSRGSGSDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTKLEIKR 128

RESULT 8
ID KY1R_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
D 01-KAPPA CHAIN V-I REGION (WEA).
D 01-HOMO SAPIENS (HUMAN).
OC ENKAROTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81098966.
RA BENTLEY D.L.; RABBITTS T.H.;
RL NATURE 288:730-733(1980).
DR EMBL; J00245; G185982; -.
EMBL; Z00001; G33196; -.

Query Match 52.6%; Score 536; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 4.48e-99;
Matches 72; Conservative 20; Mismatches 16; Indels 0; Gaps 0.

Db 1 D10MT0SPSSLSASVGDVATITCRASGIRINDLWY0OKRPGTAPKRLIYGATSSLOSQVPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 21 D10MT0SPSSLSASL6GRVAT1SCASG0D1GIN1HML0Q0EPDGT1KRLIYATSSLSGCVPK 80
1 RFSGSGCTEFTLTINSLOPEDFATYYCLOYSSFPWTGFGCTKVEVKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 81 RFSGSRGSGSDYSLTSSLESEDFVAYYCLOYASSPYTFGGGTKLEIKR 128

RESULT 9
ID KY1J_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
D 01-KAPPA CHAIN PRECURSOR V-I REGION (HK102) (FRAGMENT).
D 01-HOMO SAPIENS (HUMAN).
OC EUKAROTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81098966.
RA BENTLEY D.L.; RABBITTS T.H.;
RL NATURE 288:730-733(1980).
DR EMBL; J00245; G185982; -.
EMBL; Z00001; G33196; -.

```

Query Match	Best Local Similarity	Matches	Score 531:	DB 1:	Length 117:
Best Local Similarity 56.2%;	Pred. No. 7.30e-96;				
Matches 73;	Conservative 26;	Mismatches 28;	Indels 3;	Gaps 3;	
Db	1	MEAPQQL-FLILMLPDTTGEIYMTQSPATLSVSPGERATLSRASAQSVSNMIAWQOK	59		
Qy	1	MGAPQAIIIGFLILL-FPGTRCDIQMTQSPSSLSAIGRVSILTCRASQDIGINLHWQOE	59		
Db	60	PQGPRLIIYGASTATGIPARFSGSGGCTFTLTISLQSEDAVAYYCOQYNNMPMTE	119		
Qy	60	PQGTIKRLIYATISLSGSGVPRFSGSRGSDSYSLTISLSEDEVAIYCCLOYAS-SPTTF	118		

FT	DOMAIN	77	108	FRAMEWORK 3.
FT	DOMAIN	109	>115	COMPLEMENTARITY-DETERMINING 3.
FT	DISULFID	43	108	BY SIMILARITY.
FT	NON_TER	115	115	
SO	SEQUENCE	115 AA:	12986 MM:	958689AF CRC32:
Query Match				
Best Local Similarity		51.3%;	Score 523;	DB 1; Length 115;
Matches		74; Conservative	13; Mismatches	28; Indels 0; Gaps 0;
Db	1 MRTAQLGLILLMFPEIKCDIKMTQSPSSMVASLSEGRITCKASQDINSLVFWQKP 60			
Qy	1 MGAQAQIGLFLFFLPETRCIDIQTQSPSSLSLQRPVSLTRASQDIGINLHWLQEP 60			
Db	61 GKSEKTLIYRNLVYDGVPSRFGSGSGGQDYSLTISLEYEDMGIIYCYQYDEFP 115			
Qy	61 DGTIKRLIYATSSLSGSGVPKRFSSRSRSGSDYSLTISLSEDEVVAIYCYQYASSP 115			
RESULT 13				
ID	KV5Q.MOUSE	STANDARD;	PRT;	108 AA.
AC	P01650;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-V REGION (DPC 61).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA, METAFAA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
NC	EUTHERIA; RODENTIA.			
RP	[1]			
RP	SEQUENCE.			
RX	MEDLINE; 79195288.			
RA	VRANA M., RODIKOFF S., POTTER M.;			
RL	J. IMMUNOL. 122:1905-1910(1979).			
CC	-I- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND			
CC	BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).			
PIR	A01929: KIMS61.			
DR	HSP, P01607; 1EVD.			
KW	IMMUNOGLOBULIN V REGION.			
FT	DOMAIN	1	23	FRAMEWORK 1.
FT	DOMAIN	24	34	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	35	49	FRAMEWORK 2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	57	88	FRAMEWORK 3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	98	108	FRAMEWORK 4.
FT	DISULFID	23	88	BY SIMILARITY.
FT	NON_TER	108	108	
SO	SEQUENCE	108 AA:	11809 MM:	A5B3F462 CRC32:
Query Match				
Best Local Similarity		50.9%;	Score 519;	DB 1; Length 108;
Matches		71; Conservative	17; Mismatches	20; Indels 0; Gaps 0;
Db	1 DYQMIDSPSSLSASLDIVYTMTCASQGTSLNLMFOQPKGAKRLIYGASILEDVPS 60			
Qy	21 DIQMGTSPSSLSASLGQRYSLCTRASQDIGINLHWLQEPDGTIKRLIYATSSLSGVPK 80			
Db	61 RRSGRSGYDFTLTITSSLEDEMATYFCLQSLYLPYTTGGGTRKLEIR 108			
Qy	81 RRSGRSGSDYSLTITSSLESEDEVAIYCYQYASSPYTGGGTRKLEIR 128			
RESULT 14				
ID	KV3M.HUMAN	STANDARD;	PRT;	129 AA.
AC	P18136;			
DT	01-NOV-1990 (REL. 16, CREATED)			
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA, METAFAA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
NC	EUTHERIA; PRIMATES.			

Search completed: Thu Apr 15 17:56:44 1999
Job time : 11 secs.


```

RN [1]
RP SEQUENCE FROM N.A.
RA RYU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; 066190; G1778126; -.
PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 >131 MONOCIONLM ANTI BODY KAPPA CHAIN VARIABLE
FT NON_TER 131 131 REGION.
SQ SEQUENCE 131 AA; 14126 MW; AF1C5603 CRC32;

Query Match
Best Local Similarity 56.9%; Score 525; DB 4; Length 131;
Matches 74; Conservative 26; Mismatches 27; Indels 3; Gaps 3;

Db 3 MGAPADL-FLLLMLPDATGEIVLTQSPPTLSLSPERATFCRASQSYSGSLAMVYQ 61
1 MGAPADLGLFLLP-FPGTCDIOMTQSPSSLASLGQVSLTCRASQDI-GINLHMLQ 58
OY 59 EPGGTRKRLIYATSSLSGVPKRFSGSGSDYSLTISSEDFVAYYCLQYASSPYTF 118
Db 122 GPGTKVDIKR 131
OY 119 GGGTKLEIKR 128

RESULT 3
ID 035842 PRELIMINARY; PRT; 262 AA.
AC 035842;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HYBRIDOMA;
RX MEDLINE; 96211469.
RA SHAHREN F., DUAN L., ZHU M., BAGASRA O., POMERANTZ R.J.;
RL EMBL; 048716; G2289026; -.
PFAM; PF00047; 19.
KW RNA-DIRECTED DNA POLYMERASE.
SQ SEQUENCE 262 AA; 27842 MW; AF24DBF6 CRC32;

Query Match
Best Local Similarity 50.7%; Score 517; DB 11; Length 262;
Matches 80; Conservative 20; Mismatches 24; Indels 2; Gaps 2;

Db 2 DIIMTOSPATLSTPGDRVSLSCRASQISDFLHWYQKSHESPRLIKYASQSI-SGIP 60
OY 21 DIOMTQSPSSLASLGQVSLTCRASQDIGINLHMLQEPDGTIKRLI-YATSSLSGVP 79
Db 61 SRFGSGSGDFTLTISNVEPDVGVYCONGSHFPLTFAGTKLELRADAAPVYSIFP 120
OY 80 KRFGSGSGSDYSLTISSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTYSTFP 139
Db 121 PSSKLG 126
OY 140 PSSKLG 145

RESULT 4
ID 015982 PRELIMINARY; PRT; 116 AA.
AC 015982;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

```

```

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE RHEUMATOID FACTOR C6 LIGHT CHAIN (FRAGMENT).
GN V<KAPPA>1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RL ARTHRITIS RHEUM. (MUNCH.) 36:380-388(1993).
DR EMBL; 556182; G298561; -.
PFAM; PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 116 AA; 12528 MW; BFFBD90D CRC32;

Query Match
Best Local Similarity 50.0%; Score 510; DB 4; Length 116;
Matches 74; Conservative 19; Mismatches 22; Indels 0; Gaps 0;

Db 1 DIOMTQSPSSLASVGDVYITTCRASQISSWLAMYQKPKAPKLLIYKASSLSGVP 60
OY 21 DIOMTQSPSSLASLGQVSLTCRASQDIGINLHMLQEPDGTIKRLIYATSSLSGVPK 80
Db 61 RFGSGSGDFTLTISLQDDPATYTCQYNSIEGTFGGKVEIKRTVAPSV 115
OY 81 RFGSGSGSDYSLTISSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTY 135

RESULT 5
ID 014540 PRELIMINARY; PRT; 113 AA.
AC 014540;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB 027-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PBL;
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AB006849; D1023047; -.
PFAM; PF00047; 19.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12383 MW; FCEB1F02 CRC32;

Query Match
Best Local Similarity 49.9%; Score 508; DB 4; Length 113;
Matches 71; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Db 3 ELQMTQSPSLPASYVDRTITTCRASQITNSYLNWYQKPKAPKLLIYKASSLSGVP 62
OY 21 DIOMTQSPSSLASLGQVSLTCRASQDIGINLHMLQEPDGTIKRLIYATSSLSGVPK 80
Db 63 RFGSGSGDFTLTISLQDDPATYTCQYNSIEGTFGGKVEIKRTVAPSV 111
OY 81 RFGSGSGSDYSLTISSEDFVAYYCLQYASSPYTFGGTKLEIKRA 129

RESULT 6
ID 000619 PRELIMINARY; PRT; 134 AA.
AC 000619;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE REV25-2 (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]

```

RC	TITUS-DPL;
RA	TIOR K., SUZUKI T.;
RL	SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR	EMBL; AB006842; D1023041; -
DR	PfAM; PF00047; Ig.
FT	NON_TER .113 .113
SO	SEQUENCE .113 AA; 12207 MW; A546C704 CRC32;
 Query Match 48.2%; Score 491; DB 4; Length 113; Best Local Similarity 64.2%; Pred.No.7,44e-86; Matches 70; Conservative 20; Mismatches 19; Indels 0; Gaps 0;	
Dd	3 ELVQTSPSSLSIAASVDGRVTFTCRASOSISSYLNMTQKFGKAPKLIIYAASSLGSVPS 62 :: :::::::::::::::::::: Oy 21 DIQMTPSSSLIASIGRVSLTCRASODIGINLHWLOQEPDGTIKRILYATSSIGSVPK 80
Dd	63 RFSSGSGDTFLLTISLOPEDFAITYCCOOSYPITFFGGTKLEIRK 111 ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: Oy 81 RFSGSRSQSDYSLTISLSEDFAYVICLOYASSPYTFGGTGKLEIKRA 129
 RESULT 9 PRELIMINARY; PRT; 239 AA. ID O43690 AC O43690; DT 01-JUN-1998 (TREMBLREL. 06, CREATED) DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DE ANTI-MPL SCFY (FRAGMENT). OS HOMO SAPIENS (HUMAN). OC EUKARYOTA; METAACO; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; PRIMATES. RN [1] RP SEQUENCE FROM N.A. RA GODDARD A., YUAN J., ZHU Z., CARTER P.; RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. DR EMBL; AF048775; G2911502; -. FT NON_TER .1 1 FT NON_TER .244 244 SQ SEQUENCE .239 AA; 25262 MW; 5B9ABF4C CRC32;	
 Query Match 48.1%; Score 490; DB 4; Length 239; Best Local Similarity 65.4%; Pred.No.1,28e-85; Matches 70; Conservative 18; Mismatches 19; Indels 0; Gaps 0;	
Dd	133 DIOMTQSPSTLSAISIGNRVITTCASAGCIYHMLAMYQRKGAKPCLLIYASSLASGAPS 192 ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: Oy 21 DIQMTPSSSLIASIGRVSLTCRASODIGINLHWLOQEPDGTIKRILYATSSIGSVPK 80
Dd	193 RFSSGSGDTFLLTISLOPDPAIVCYCOQSYNPFLFFGGTKLEIR 239 ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: Oy 81 RFSGSRSQSDYSLTISLSEDFAYVICLOYASSPYTFGGTGKLEIKR 127
 RESULT 10 PRELIMINARY; PRT; 244 AA. ID O43689 AC O43689; DT 01-JUN-1998 (TREMBLREL. 06, CREATED) DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) DE ANTI-HERS SCFY (FRAGMENT). OS HOMO SAPIENS (HUMAN). OC EUKARYOTA; METAACO; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; PRIMATES. RN [1] RP SEQUENCE FROM N.A. RA GODDARD A., YUAN J., ZHU Z., CARTER P.; RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. DR EMBL; AF048774; G2911500; -. FT NON_TER .1 1 FT NON_TER .244 244 SQ SEQUENCE .244 AA; 26025 MW; 47670049 CRC32;	
Query Match 48.1%; Score 490; DB 4; Length 244;	

Query Match	47.1%;	Score 480;	DB 11;	Length 107;
Best Local Similarity	65.4%;	Pred. No. 2.77e-83;		
Matches	70;	Conservative	11;	Mismatches 26; Indels 0; Gaps 0;

```
Db      1 DIVMTQSOTFNSTSVGDVRSVYTCASQNNVTNVAWYOQKPGQSPKALITYSASYPYSGVP 600
        ||||| : ::||::||::||::||: | : || : | ||:::| ||||
Qy     21 DIQMTPSSLSASLGGRVSLTRASQDIGINLHMTQQEPPDTIKRLIYATSSLSGVPK 800
```


THIS PAGE BLANK (USPTO)

QY 163 TGGCTAAGACAGACACCTGGACAGGGCGCTGCATGGATGGATGGAAATATTTTCTTCGTGGAAAT 222
Db 197 GGTAGACAAACCTTTGACGGAGTTTTCAGAGACAGAGTCAAGCTTGACCACTGACATCC 256
QY 223 GGTATCTACTACTACATCATCAGAAAGTTTAAAGCGCAAGGCCCTCATGTCATCACAACATCC 282
Db 257 ACGAATACAGCCTCATCATGAGAGCTGAGAACTCATGATCTGACAGACAGCGCCATATATTC 316
QY 283 TCCAGCACAGACCTTCATCATCGATCAGATCAGCCTCATCATCTGAAAGACTCTCGGGCTATATTC 342
Db 317 TGTGCGAGAG 326
QY 343 TGTGCAAGAG 352

RESULT 7
LOCUS 238 bp mRNA EST 06-SEP-1995
DEFINITION EST898669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain V region (GB:X61012) (HT:3230).
STION 729670
 9611768
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Small Intestine.
ORGANISM Homo sapiens

REFERENCE
 Adams M.D., Kerlavage A.R., Fleischmann R.D., Fulmer R.A., Bult C.T., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., Fitzhugh W.M., Fritchman J.T., Geoghegan N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Kimble K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Seudek D.M., Shirley R., Small K.V., Spriggs T.A., Uterback T.R., Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Dimke D., Feng P., Fertie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber D., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meisner P.S., Olsen H., Raymond L., Welty F.F., Wang J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Hesselting W.A., Fields C., Fraser C.M. and Venter J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns Based upon 52 Million Basepairs of cDNA Sequence unpublished (1995)

TITLE
JRNAL
COMMENT
 Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@db.tigr.org
 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).
 Location/Qualifiers
 1. 238
 /organism="Homo sapiens"
 <1..>238
 46 a 70 c 69 g 52 t 1 others

FEATURES
 source
 mRNA
 BASE COUNT
 ORIGIN
 Query Match 20.6%; Score 95; DB 16; Length 238;
 Best Local Similarity 74.2%; Pred. No. 1,17e-139;
 Matches 144; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

43 ATGACATGACCTGAGACATCTTTTNTGTGGCAGCAGCAACAGTCCCACTCCAG 102

QY	1	ATGGAATCAGATGGGTCTTTCTCTTCCTCCCTGTCGTAATACACAGAGTGTCCACTGCCAG	60
Db	103	GTTACGCTGCTGTCACCTCTGCAGCTAGAGTGAAGAAGCCCTGGGCGCTCACTGAAGCTTCC	162
QY	61	GCTATTCACACAGACTCTGGGCGCTAGCTGTGCAGAGCTGTGGGCGCTCATGTGAAGATGTC	120
Db	163	TGCAGGCTTCTGGTTACACCTTTCACGACTCCGGTATTCAGCTGGTGGTGCAGAGGCCCT	222
QY	121	TGCAGGCTTCTGGCTACACATTTGACACAGTTTCAATATGCTGGGTAAAGACAGACACT	180
Db	223	GGACAGAGGCTTTGA	236
QY	181	GGACAGGCGCTTGA	194
RESULT	8		
LOCUS	AA377128	265 bp	mRNA
DEFINITION	EST89660	Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ region, mRNA sequence.	
ACCESSION	AA377128		
NID	92029456		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 265)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weissstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,A.L., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL MEDLINE COMMENT	Nature 377 (6547 Suppl), 3-174 (1995)		
OTHER ESTS	THC167579		
CONTACT	Kerlavage, AR		
Bioinformatics	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arkerlav@tigr.org		
	For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)		
	Seq primer: M13 Reverse.		
FEATURES	location/qualifiers		
SOURCE	1..265		
	/organism="Homo sapiens"		
	/note="Organ: small intestine; Vector: pluescript SK-; Site_1: EcoRI; Site_2: XhoI"		
	/db_xref="ATCC (inhost):181546"		
	/db_xref="taxon:9606"		
	/clone_lib="Small intestine I"		
	/dev_stage="adult"		
	<1..>265		
MRNA	57 a	69 c	79 g
BASE COUNT	58 t	2 others	
ORIGIN			

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTTCACATCTGAGAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:10090"
/clone="1398374"
/clone_lib="Soares mouse mammary gland NbMAG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

BASE COUNT 38 a 32 c 25 g 21 t

Query Match 18.7%; Score 86; DB 17; Length 116;
Best Local Similarity 89.1%; Pred. No. 4,46e-121;
Matches 98; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 2 AGAAGTTCAGAACAGCCACACTGACAGACAATCTCCAGACAGCCTACATGC 61
|||||
Oy 242 AGAAGTTTAAAGGGAGCGCTCATTTGACAGACATCTCCAGACAGCCTACATGC 301
|||||
Db 62 AACTCGACAGCCTGACATCTGAGACACTGGCTTATTACTGTGGAAGA 111
|
Oy 302 AGATCGACAGCCTGACATCTGAGACACTGGCTTATTACTGTGGAAGA 351
|

RESULT 11
LOCUS AA987559 336 bp mRNA EST 23-JUL-1998
DEFINITION or83g01.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1602480 3'
similar to gb:U87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
sequence.
ACCESSION AA987559
NID 93172923
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 336)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Koskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdnp/image/image.html

Insert Length: 801 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amerisham
High quality sequence stop: 322.
Location/Qualifiers
1..336
/organism="Homo sapiens"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
neuroendocrine lung carcinoma, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="IMAGE:1602480"
/clone_lib="NCI-CGAP Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"

BASE COUNT 82 a 86 c 100 g 68 t

Query Match 18.4%; Score 85; DB 15; Length 336;
Best Local Similarity 63.8%; Pred. No. 5.00e-119;
Matches 197; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Db 14 ACAGTCTCCAGTCACAGCTCCAGATGAGAACACTAGGGCGTGAAGAACAGG 73
|||||
Oy 43 ACAGGTCTCCAGTCCAGCTCCAGCTTATCTACAGCAGTGTGGGTGAGCTGG 102
|||||
Db 74 TCTTCGTAAGGTGACCTGCTTGGCTTGGAGGACCTTCGGTGTGACTGCAC 133
|
Oy 103 GCCTCAGTAAGATGCTCTGCAAGGCTTGTGCTACACATACCATATAGCAC 162
|
Db 134 TGGGTGCGACAGGCGCTTGACACAGCGCTGAGTGGAGGGAAGATCCCATCGT 193
|||||
Oy 163 TGGGTAAACAGACACCTGAGACAGGCGCTGGAATGATGGAATTTTCTCGGAAT 222
|
Db 194 CATTCAGCACTACGACACCAAGTTTTCAGACAGATACATAACCGGCAATCT 253
|
Oy 223 GGTGATCTTACTACATGATGAAGTTTAAGGGCAAGCGCTCATGCTCAACACATCC 282
|
Db 254 ACGGCTCAGTCTACATGGAATGACACAGCTGATTTTGAAGACGCGCATATATAT 313
|
Oy 283 TCCAGACAGCCTACATGAGATGACACAGCCTGACATCTGAAGACTCTCGTATTTC 342
|
Db 314 TGTGCGAGA 322
|
Oy 343 TGTGCNAGA 351
|

RESULT 12
LOCUS T28938 209 bp mRNA EST 06-SEP-1995
DEFINITION EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu
heavy chain, VDJ regions (GB:M17751) (H:3055).
ACCESSION T28938
NID 9611036
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human White blood cells.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 209)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weissbrock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle, Hughes, J., Fine, L.D.,
Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghegan, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P.S.,
Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marrairos, S.M.,
Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudke, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utechtack, T.R.,
Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferlie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wang, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, K.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE	Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL	Based Upon 52 Million Basepairs of cDNA Sequence
COMMENT	Unpublished (1995)

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Tel: 3018699423
Fax: 3018699423
Email: j.venter@igbmc.org

FEATURES	Location/Qualifiers
Source	1 300

	BASE COUNT	OP	RNA	OP	BASE COUNT	OP	RNA
43	a	62	c	48	g	55	t
1	others						

Db	2	GGAGTGTTCCTGGTAAAGTGAGCACTCCCTGGACACTTGTAAATTTGGTTAC	61
Cp	282	GGATGTGTCTGCAGTCAATGAGGCTTCCCTTAAACTTCTGATTGTGTAATCAC	223
Db	62	ATTGCCAGCGTTGATCCATCCATCCACTCAAGCCTTGTCCGGGGGCGCTGGCCACCA	121
Cp	222	ATTTCACGAAATAATTTTCCATTCATTCACAGGCGCTGCAGAGTGTCTCTTAACCA	163
Db	122	ATGATACACAGCTAGTGAAGGTGTATCCGAAAGCCTTGCAGGAACTTCACTGAGGC	181
Cp	162	GTGATATTGTAACTGTGTCATGTGTACCCAGAGCCTTGCAGGACATCTTCACTGAGGC	103
Db	182	CCGAGCGTTTCTACCTAGGCC	204
Cp	102	CCGAGACCTCACAGCTTAGGCC	80

LOCUS	RESULT
AA710970	431 bp mRNA EST 24-DEC-1997
v693h09.1	Soares mouse mammary gland NbMMG Mus musculus cDNA clone
i178753.5	similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:x70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);, mRNA sequence.
U140625	

ACCESSION	AA710970
NUMBER	92720888
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus. (bases 1 to 431)

REFERENCE
AUTHORS
1 (bases 1 to 431)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gaisel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Weinstein, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)

Contact: Maira M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:636601

```
Seq primer: -28ml3 rev2 ET from AmerSham
High quality sequence stop: 198.
Location/Qualifiers
1. .431
```

constructed and normalized by Bento Soares and Ronaldo."

`/db_xref="taxon:10090"`

`/clone="1178753"`

BASE COUNT	112 a	103 c	112 g	104 t
ORIGIN				

Query Match	16.3%;	Score 75;	DB 11;	Length 431;
Best Local Similarity	61.2%;	Pred. No. 1.00e-98;		
Matches 205; Conservative	0;	Mismatches 130;	Indels 0;	Gaps 0;

[illegible]

RESULT	14		
LOCUS	AA383972	198 bp	mRNA
DEFINITION	EST974423 Thymsus II Homo sapiens CDNA 5' end similar to immunoglobulin heavy chain, VDJ regions (CB:214165), mRNA sequence		
ACCESSION	AA383972		
NID	92036290		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE
AUTHORS

1 (Pages 1 to 198)

Adams, M.D., Kerlawage, A.R., Fleischmann, R.D., Fulmer, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-
gla, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

THIS PAGE BLANK (USPTO)

DR WPI: 97-341690/31.
 DR N-PSDB: T85149.
 PR Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 PR against human milk fat globule disease associated tumours,
 PR especially breast cancer.
 PS Claim 9: Page 94: 130pp: English.
 CC This polypeptide sequence comprises the light chain variable region
 CC (VL) of monoclonal anti-idiotypic antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with MC-10 anti-HMG antibody to obtain an anti-idiotypic
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides (see also T85149-50) are claimed.
 CC Also claimed are diagnostic kits and methods of using 11D10, 11D10
 CC polypeptides and/or 11D10 polynucleotides, including methods of
 CC treating HMG-associated tumours. 11D10 is also used in a claimed
 CC method of palliating HMG-associated disease and in claimed kits to
 CC detect or quantify anti-HMG antibody.
 SQ Sequence 145 AA:

Query Match 100.0%; Score 1019; DB 25; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1,136-66;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 mgapagifglllllfpqrcdigmqspsslsaslgvslcrasqdglnhwlqgqp 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 1 MGAPAGIIGFLLLPFGTCIDIOMTQSPSSLSASLGQRSLCRASQDGINHMLQDGP 60
 DB 61 dgtkrllyatslsgvypkrfsgsrsgdysltsslesedfyaycylqyasspytfgg 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 DGTIKRLIYATSSLSGSGVPKRFGSGRSGSDYSLTSSLESDFVAYYCLQYASSPYTFGG 120
 DB 121 gtkleikrdaapvtsifpssklg 145
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 GTKLEIKRADAPVTSIFPSSKLG 145

RESULT 2
 ID P30251 standard; peptide: 146 AA.
 AC P30251.

DE 25-MAY-1992 (first entry)
 DE Sequence of the leader, variable region and first 16 AAs of
 DE the constant region of the kappa-chain (light chain) of MOPC1.
 DE Diagnosis: therapy; immunoglobulin.

EH Homo sapiens.
 FH Key Location/Qualifiers
 FT region 1..22
 FT /label= leader
 FT region 23..130
 FT /label= variable
 FT region 131..146
 FT /label= constant

PN EP-88994-A.
 PD 21-SEP-1983.
 PF 10-MAR-1983: 001655.
 PR 15-MAR-1983: US-358414.
 PR 05-DEC-1983: US-558551.
 PA (SCHE) SCHERING CORP.
 PA (DNAX-) DNAX RES INST.
 PI Moore KW, Zaffaroni A;
 DR WPI: 83-772290/39.
 DR N-PSDB: N30165.

PT Transformed expression vectors or plasmid(s) - with double
 PT stranded DNA sequence coding only for desired part of polypeptide
 PT chain.
 PS Example: Page 40-41: 68pp: English.
 CC The pref. vector or plasmid of the invention has a double-stranded
 CC DNA seq. coding for a variable region of a light or heavy chain of
 CC IgG, or for a variable region of a light or heavy chain of an
 CC immunoglobulin specific for an enzyme or surface protein. The

CC sequence esp. codes for a variable region of a light chain having 95-
 CC 115 AAs or for a variable region of a heavy chain having 110-125 AAs
 CC seq. including the D region of the heavy chain.
 SQ Sequence 146 AA:

Query Match 90.2%; Score 919; DB 4; Length 146;
 Best Local Similarity 92.3%; Pred. No. 4,636-59;
 Matches 131; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

DB 3 mrpavhvfqlllllfpqrcdigmqspsslsaslgvslcrasqdglnhwlqgqp 62
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 1 MGAPAGIIGFLLLPFGTCIDIOMTQSPSSLSASLGQRSLCRASQDGINHMLQDGP 60
 DB 63 dgtkrllyatslsgvypkrfsgsrsgdysltsslesedfyaycylqyasspytfgg 122
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 DGTIKRLIYATSSLSGSGVPKRFGSGRSGSDYSLTSSLESDFVAYYCLQYASSPYTFGG 120
 DB 123 gtkleikrdaapvtsifpss 144
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 GTKLEIKRADAPVTSIFPSS 142

RESULT 3
 ID W22537 standard; protein: 129 AA.
 AC W22537.

DE 03-NOV-1997 (first entry)
 DE Murine anti-human class II monoclonal antibody 44H104 VL chain.
 DE Antibody: light chain; variable region; hybridoma cell line 44H104;
 DE immune response; enhance; stimulate; vaccine; immunodiagnosis;
 DE antigen delivery.

OS Mus musculus.
 PN W09640941-A1.
 PD 19-DEC-1996.
 PF 07-JUN-1996: CA0400.
 PR 07-JUN-1995: US-483576.
 PA (CONN-) CONNACU GHT LAB LTD.
 PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
 DR WPI: 97-077271/07.
 DR N-PSDB: T77851.

PT Recombinant conjugate antibody mol., modified for delivering an
 PT antigen - elicits enhanced immune response without the use of
 PT adjuvant to generate antibodies which are useful in vaccines or
 PT immuno:diagnosis

PS Example 1: Fig 1A: 64pp: English.
 CC Novel recombinant conjugate antibody molecules comprise a monoclonal
 CC antibody specific for a surface structure of antigen presenting
 CC cells (APC), genetically modified to contain at least one antigen
 CC exclusively at one or more preselected sites. The conjugate is capable
 CC of delivering the antigen to APC and eliciting an immune response to
 CC the antigen. The new conjugates are useful as vaccines and are able
 CC to elicit an enhanced immune response without the use of an adjuvant.
 CC In a specific example, a conjugate was constructed using the murine
 CC anti-human class II monoclonal antibody secreted by hybridoma
 CC 44H104. The peptide CTRB36 was chosen as antigen; it consists of
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.
 CC The present sequence represents the light chain variable region
 CC from 44H104 which was used in the preparation of a conjugate with
 CC antigen CTRB36.
 SQ Sequence 129 AA:

Query Match 74.0%; Score 754; DB 24; Length 129;
 Best Local Similarity 81.1%; Pred. No. 1,496-46;
 Matches 103; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

DB 3 mrpavhvfqlllllfpqrcdigmqspsslsaslgvslcrasqdglnhwlqgqp 62
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 1 MGAPAGIIGFLLLPFGTCIDIOMTQSPSSLSASLGQRSLCRASQDGINHMLQDGP 60
 DB 63 dgtkrllyatslsgvypkrfsgsrsgdysltsslesedfyaycylqyasspytfgg 122
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 DGTIKRLIYATSSLSGSGVPKRFGSGRSGSDYSLTSSLESDFVAYYCLQYASSPYTFGG 120
 DB 123 gtkleik 129

```

Oy      121 GPKLEIK 127

RESULT 4
ID      R39569 standard; Protein; 246 AA.
AC      R39569;
DT      07-FEB-1994 (first entry)
DE      Sequence of 520C9 sfv protein.
KW      Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW      biosynthetic single polypeptide chain binding site; ss.
OS      Synthetic.
PN      WO9316185-A.
PD      19-AUG-1993.
PE      05-FEB-1993.
PR      06-FEB-1992; US-831967.
PA      (CETU) CETUS ONCOLOGY CORP.
PA      (CREA-) CREATIVE BIOMOLECULES INC.
PI      Houston TX, Houston JS, Oppermann H, Ring DB;
PI      WPI: 93-272889/34.
DE      N-PSDB: Q46084.
SQ      New single chain Fv polypeptide binding to C-erbB-2 tumour
        antigen - for imaging or treating breast or ovarian cancer etc.
PS      Claim 4; pages 60-61; 87pp; English.
CC      C-erbB-2 refers to a protein antigen expressed on the surface of
CC      tumour cells, such as breast and ovarian tumour cells, which is an
CC      approx 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC      pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sfv)
CC      is a covalently linked VH-VL heterodimer which is expressed from
CC      a gene fusion including VH- and VL- encoding genes connected by
CC      a peptide-encoding linker. Such linker sequences are set forth in
CC      AA residues 116-135 in R39569, which includes part of the 16 AA
CC      linker sequences in R39572. Using Q46084 for the 520C9 monoclonal
CC      antibody, a single chain polypeptide can be produced having a
CC      binding affinity for a C-erbB-2 related antigen. 'X' in R39569
CC      refers to the location of a stop codon in Q46084.
SQ      Sequence 246 AA;

Query Match      69.2%; Score 705; DB 8; Length 246;
Best Local Similarity 89.4%; Pred. No. 7.40e-43;
Matches 101; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db      134 d1qmtqspsslsaslgervsltrcrasqdgslw1qgpepdtlkrilyatslsgvpx 193
Oy      21 DIQMTPSSLSASLGQRVSLTRCRASQDIGNLHMLQGPDPGTRRLRYATSSLSGVPK 80
        |||||||
Db      194 rfsgrsgdyslttslesgdffvvyqlqyalfpytfggtflektradaa 246
Oy      81 RFGSGRSGDYSLTSSLESEDFVAYVCLQYASSPYTREGGKLEIKRADAA 133
        |||||||

RESULT 5
ID      W27121 standard; Protein; 107 AA.
AC      W27121;
DT      04-JAN-1998 (first entry)
DE      Murine antibody light chain variable region consensus.
KW      Monoclonal antibody 1D10; anti-idiotype antibody; mucin;
KW      human milk fat globule; HMG; tumour; breast cancer; vaccine.
OS      Mus musculus.
PI      Key
PI      Location/Qualifiers
PI      Region
PI      24..34
PI      /label= CDR1
PI      /note= "complementarity determining region 1"
PI      50..56
PI      /label= CDR2
PI      /note= "complementarity determining region 2"
PI      88..96
PI      /label= CDR3
PI      /note= "complementarity determining region 3"

PN      WO9722699-A2.
PD      26-JUN-1997.
PE      19-DEC-1996; US-575762.
PR      13-DEC-1996; US-575762.

```

```

PR      20-DEC-1995; US-575762.
PR      26-JAN-1996; US-591965.
PA      (KERT) UNIV KENTUCKY.
PI      Chatterjee M, Chatterjee SK, Foon KA;
PI      WPI: 97-341690/31.
DE      Monoclonal anti-idiotype antibody 1D10 - elicits immune response
DE      against human milk fat globule disease associated tumours,
DE      especially breast cancer
PS      Example 2; Fig 28C; 130pp; English.
CC      This polypeptide sequence comprises a consensus sequence of murine
CC      light chain variable regions (VL) selected on the basis of identity
CC      to the VL region (see W27119) of monoclonal anti-idiotype antibody
CC      1D10. The sequences were obtained from a Genbank database
CC      search. A VH consensus (W27122) was also produced. 1D10 has at
CC      least 18 departures from the consensus sequences (7 in the light
CC      chain and 11 in the heavy chain). 8 occur within CDRs and 10
CC      outside CDRs. 1D10 polypeptides and polynucleotides can be
CC      used in vaccines and pharmaceutical compositions for the treatment
CC      of human milk fat globule-associated diseases such as breast
CC      cancer.
SQ      Sequence 107 AA;

Query Match      68.9%; Score 702; DB 25; Length 107;
Best Local Similarity 93.5%; Pred. No. 1.25e-42;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db      1 d1qmtqspsslsaslgervsltrcrasqdgslw1qgpepdtlkrilyatslsgvpx 60
Oy      21 DIQMTPSSLSASLGQRVSLTRCRASQDIGNLHMLQGPDPGTRRLRYATSSLSGVPK 80
        |||||||
Db      61 rfsgrsgdyslttslesgdffvvyqlqyasspytfggtflek 107
Oy      81 RFGSGRSGDYSLTSSLESEDFVAYVCLQYASSPYTREGGKLEIK 127
        |||||||

RESULT 6
ID      W02280 standard; Protein; 243 AA.
AC      W02280;
DT      29-OCT-1996 (first entry)
DE      520C9 anti-C-erbB-2 two single chain Fv construct.
KW      520C9; anti-C-erbB-2 monoclonal antibody; single chain Fv; sfv;
KW      construct; polypeptide linker; C-terminal amino acid sequence;
KW      in vivo imaging; drug targeting experiment; homodimer;
KW      Homo sapiens.
OS      Homo sapiens.
PI      Key
PI      Location/Qualifiers
PI      peptide 118..133
PI      /label= linker

PN      US5534254-A.
PD      09-JUL-1996.
PE      06-FEB-1992; 831967.
PR      06-FEB-1992; US-831967.
PR      07-OCT-1993; US-133804.
PA      (CHIR) CHIRON CORP.
PA      (CREA-) CREATIVE BIOMOLECULES INC.
PI      Houston TX, Houston JS, Oppermann H, Ring DB;
PI      WPI: 96-333194/33.
DE      N-PSDB: R36880.
DE      Compns. contg. antigen-targeting antibody fragment constructs -
DE      comprising dimer of single-chain Fv fragments
PS      Example 1; Columns 33-36; 30pp; English.
CC      Variable heavy (VH) and variable light (VL) genes were cloned from
CC      a 520C9 hybridoma cDNA library, using probes directed toward the
CC      antibody constant and joining regions. A two single chain Fv (sfv)
CC      gene was constructed by connecting the VH and VL genes with a
CC      Ser rich polypeptide linker. The resulting 520C9 two sfv gene,
CC      which encodes the present sequence, was inserted into an expression
CC      vector, transformed into E. coli, and protein expression induced by
CC      the addn. of IPTG to the culture medium.
CC      A compsn. comprising a carrier and drug targeting experiments. The
CC      2 sfv protein prod. is a homodimer, in which both fragments target
CC      the same antigen, therefore giving greater binding avidity and

```

CC longer tissue retention times, compared to individual sFv protein
CC prod. fragments.
SO Sequence 243 AA;

Query Match 68.9%; Score 702; DB 18; Length 243;
Best Local Similarity 91.8%; Pred. No. 1,256-42;
Matches 101; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 134 dimgtqspssiasigervsltrcasgdlmglwlggedtllkrllyatsldsgvpx 193
|||||
Qy 21 DIOMQSPSSISASLGQVSLCRASODIGINLHWLQOEPDGTIKRLIYATSSLSGVPK 80
|||||
Db 194 rfsgrsrsdylstlslesedfvvvyqlayalfyftgggnleikrad 243
|||||
Qy 81 RFSGRSSDYLSTISSLESEDFVAYVCLQYASSPYRFGGKLEIKRAD 130
|||||

LT 7
R15322 standard; Protein; 144 AA.
R15322:

DT 16-MAR-1992 (first entry)
DE IL-2 chimeric antibody light chain.
KW Interleukin-2; immunosuppressant.
OS Chimeric Homo sapiens.
FH Chimeric Mus musculus.

FT Key Location/Qualifiers
FT peptide 1..20
FT peptide /note= "signal peptide"

FT peptide 21..115
FT peptide /note= "V-region"

FT peptide 116..127
FT peptide /note= "J1-region"

FT peptide 128..144
FT peptide /note= "C-region"

PN EP-460674-A.
PD 11-DEC-1991.
PR 06-JUN-1991; 109303.

PR 08-JUN-1990; DE-018442.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Weidle U, Kaluza B, Knapp W;
DR WPI; 91-363168/50.
DR N-PSDB; 015114.

PT New recombinant DNA encoding chimeric antibody - with human
PT constant and non-human variable regions, esp. directed against
PT interleukin 2 receptor

PT Disclosure; Page 11; 24pp; German.
PT The sequence is that of the interleukin-2 (IL-2) chimeric antibody
light chain, coded by clone 447. Antibodies against IL-2 receptors
are useful as immunosuppressants, and are much less immunogenic than
CC mouse or rat antibodies. See also R15321-R15326.
SO Sequence 144 AA;

Query Match 67.9%; Score 692; DB 3; Length 144;
Best Local Similarity 71.1%; Pred. No. 7,056-42;
Matches 101; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

Db 1 mmvjaqlafallwfpagrcdlmtqspssmsvslgdtvtltchaggsirsnlwlqgkp 60
|||||
Qy 1 MGAPAOILGFLLEFPGRCDIQMTQSPSSISASLGQVSLCRASODIGINLHWLQOEP 60
|||||

Db 61 gksfsglylnhtnledgyprsfsgsgsqdylstlslesedfadyvqvyaqfprttgg 120
|||||
Qy 61 DGTIKRLIYATSSLSGQVPKRSGSRGSDYLSTISSLESEDFVAYVCLQYASSPYRFGG 120
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

Db 121 gtlkleikradaaptyvsiifpps 142
|||||
Qy 121 GTKLEIKRADAPTVSIFPPS 142
|||||

DE Human anti-HBs light chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
OS Homo sapiens.

FT Key Location/Qualifiers
FT peptide 1..22
FT peptide /label= sig_peptide
FT protein 23..236
FT protein /label= mat_protein

PN WO9320205-A.
PD 14-OCT-1993.
PR 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Atima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
DR WPI; 93-36913/42.
DR N-PSDB; 049943.

PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
PS Disclosure; Fig 4-5; 46pp; Japanese.
CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
SO Sequence 236 AA;

Query Match 67.8%; Score 691; DB 8; Length 236;
Best Local Similarity 66.0%; Pred. No. 8,406-42;
Matches 93; Conservative 25; Mismatches 23; Indels 0; Gaps 0;

Db 3 mrvaqlllglllwfpgardimtgspasavdgrvtltcrasgdlmglwlggedtllkrllyatsldsgvpx 62
|||||

Qy 1 MGAPAOILGFLLEFPGRCDIQMTQSPSSISASLGQVSLCRASODIGINLHWLQOEP 60
|||||

Db 63 gkyprklllyaaaslgsgvperfsqsgteftllslrqpeditatyyclhnnypslsfsg 122
|||||

Qy 61 DGTIKRLIYATSSLSGQVPKRSGSRGSDYLSTISSLESEDFVAYVCLQYASSPYRFGG 120
|||||

Db 123 gtlkleikrtvaapevsiifpps 143
|||||

Qy 121 GTKLEIKRADAPTVSIFPPS 141
|||||

RESULT 9
ID R21310 standard; Protein; 108 AA.
AC R21310;

DT 21-MAY-1992 (first entry)
DE Light chain of M1f clone.

KW Fc; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW plus; gfp; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.

OS Synthetic.

FH Key Location/Qualifiers
FT region 25..34
FT region /label= CDR1
FT region 50..56
FT region /label= CDR2
FT region 89..96
FT region /label= CDR3

PN WO9201047-A.
PD 23-JAN-1992.
PR 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMP) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonfert TP;
DR WPI; 92-056862/07.

PT Producing members of specific binding pairs - by expression in

PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 46; Fig 52; 109pp: English.
CC The sequence is the light chain of clone MIF encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prep.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, pSM1-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fDCA72
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFI and M21 are given in R21310 and R21311
CC respectively. The D1.3 light chain is given in R21309.
CC See also R21260-307, 309-312, R22450, R22565, R22567-81.
SQ Sequence 108 AA;

Query Match 67.7%; Score 690; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 9,99e-42;
Matches 98; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 d1eltgsspsissalgservsltrcasqdlsslnwlgdpdgtlkrllyatssidsyvk 60
||:|||||||||||||||||||||||:|||||||||||||||||
QY 21 DIQMTGSPSSISASLGKRVSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 108
|||||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 128
QY 81 RFSGSRGSDYSLTSSLESSEDFVAYICLOAYASSPYTFGGGTKEIKRA 128

RESULT 10
ID W18271 standard; peptide; 109 AA.
AC W18271;
DE PRP 37 light chain variable region.
KW P101 protein; PRP: heavy chain variable region; antibody; scrapie;
KW light chain variable region; PRP-Sc; pathogen; fatal familial insomnia;
KW central nervous system spongiform encephalopathy; human; therapy;
KW transmissible neurodegenerative disease; Creutzfeldt-Jacob Disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW Serstman-Strassler-Scheinker Disease.
OS Mus musculus.
FT Key Location/Qualifiers
FT Region 1..23
FT Region 24..34 "framework region 1"
FT Region 35..49 "complementarity determining region 1"
FT Region 50..56 "framework region 2"
FT Region 57..88 "complementarity determining region 2"
FT Region 89..97 "framework region 3"
FT Region 98..109 "complementarity determining region 3"
FT Region 109..109 "framework region 4"
FT Region 109710505-A1.
PD 20-MAR-1997.
PE 13-SEP-1996; U14840.
PR 14-SEP-1995; US-528104.
PA (REGC) UNIV CALIFORNIA.
PI Burton DR, Prusiner SB, Williamson RA:
DR WPI: 97-202357/18.
PT New antibodies to the scrapie isoform of prion protein - used for
PT detection of infectious prion proteins or for treating disease such
PT as BSE, CJD or scrapie.
PS Example 9; Fig 6; 99pp: English.
CC W18266-W18285 represent portions of the antibodies of the invention. The
CC antibodies of the invention are able to bind the scrapie isoform of prion

CC protein PRP-Sc in situ. Prions are infectious pathogens that cause
CC central nervous system spongiform encephalopathies in humans and animals.
CC The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC the transmission and pathogenesis of the transmissible neurodegenerative
CC diseases of animals and humans. The antibodies can be used in a method of
CC the invention for detecting human PrP-Sc in a source. The antibodies
CC specifically bind to prion proteins associated with disease and do not
CC bind to denatured PRP proteins not associated with disease. They can bind
CC to prion proteins of a specific species of mammals. They can also have
CC the ability to neutralise infectious prions. The antibodies can be used
CC for screening for the presence of prions in products such as
CC pharmaceuticals, food or cosmetics. They can also be used for prion
CC neutralisation to purify products, for extraction of prion proteins or
CC for therapy for diseases such as bovine spongiform encephalopathy,
CC Creutzfeldt-Jacob Disease, fatal familial insomnia or
CC Serstman-Strassler-Scheinker Disease, scrapie or feline spongiform
CC encephalopathies.
SQ Sequence 109 AA;

Query Match 67.5%; Score 688; DB 25; Length 109;
Best Local Similarity 89.0%; Pred. No. 1.41e-41;
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 elqmtgsspsissalgservsltrcasqdlsslnwlgdpdgtlkrllyatssidsyvk 60
||:|||||||||||||||||||||||:|||||||||||||||||
QY 21 DIQMTGSPSSISASLGKRVSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 109
|||||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 129
QY 81 RFSGSRGSDYSLTSSLESSEDFVAYICLOAYASSPYTFGGGTKEIKRA 129

RESULT 11
ID R39571 standard; Protein; 534 AA.
AC R39571;
DE 07-FEB-1994 (first entry)
DE Sequence of G-FIT.
KW Tumour antigen; c-erbB-2; G-FIT.
OS Synthetic.
PN W09316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.
PA (CETU) CETOUS ONCOLOGY CORP.
PI Houston IL, Huston JS, Oppermann H, Rung DB;
DR WPI: 93-272889/34.
DR N-PSDB; Q46086.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Example; pages 65-68; 87pp: English.
CC C-erbB-2 refers to a protein expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568).
SQ Sequence 534 AA;

Query Match 67.5%; Score 688; DB 8; Length 534;
Best Local Similarity 89.1%; Pred. No. 1.41e-41;
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 425 d1qmtgsspsissalgservsltrcasqdlsslnwlgdpdgtlkrllyatssidsyvk 484
|||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 130
QY 21 DIQMTGSPSSISASLGKRVSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||fsgsrsgsdysltisslesedfvdycclygasspwtffgggtkllelra 130
QY 81 RFSGSRGSDYSLTSSLESSEDFVAYICLOAYASSPYTFGGGTKEIKRAD 130

RESULT 12
ID R15321 standard; Protein; 144 AA.
AC R15321;

Job time : 43 secs.

CC method can be used to delay the development of a variety of tumours,
 CC including colorectal, gastric and pancreatic tumours, as well as
 CC other adenocarcinomas such as those of the breast and lung, and
 CC biliary cancer, and gynaecological cancers.
 SQ Sequence 142 AA;

Query Match

Best Local Similarity 65.0%; Score 662; DB 27; Length 142;
 Pred. No. 1.28e-39;

Matches 96; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

Db 1 mvsatqflllllwfpgksdkmtqspssmyaslgervltlckasqdinglnwfgqp 60

QY 1 MGAPAOILGFLLEFPGRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHWLOEP 60

Db 61 gkspklllyranrldgypsfsgsgqvytlstssleyedmgtyclqdfefpwmfg 120

QY 61 DGTIKRLIYATSSGSGPKRFSGSGSDYSLTISLSEDFVAYCYCLOAYASSPYTFG 120

Db 121 gtlkrlkradaapvtvsifppss 142

QY 121 GTRKLEIKRADAPTVSIFPPSS 142

RESULT

ID R99686 standard; Protein; 142 AA.

AC R99686;

DT 11-OCT-1996 (first entry)

DE Monoclonal anti-Idiotypic antibody 3H1 light chain variable region.

KW Anti-Idiotypic antibody; monoclonal antibody; CEA;

KM Carcinoembryonic antigen; tumour-associated antigen; cancer;

KM vaccine; immunotherapy.

OS Mus sp.

PN NO9620219-A2.

PD 04-JUL-1996.

PE 28-DEC-1995; U17105.

PR 28-DEC-1994; US-365484.

PA (KENT) UNIV KENTUCKY.

PI Chatterjee M, Chatterjee SK, Foon KA, Kohler H;

DR WPI: 96-321809/32.

DR N-PSDB: T34541.

PT Monoclonal anti-Idiotypic antibody 3H1 - elicits an immune response

PT to carcinoembryonic antigen

PS Claim 5; Fig 1B; 102pp; English.

CC The amino acid sequence (R99686) of the light chain variable region

CC deduced from a cDNA clone (T34541) Obt. by PCR amplification

CC (see also T34545-46) of cDNA derived from 3H1 hybridoma cells.

CC Anti-Idiotypic antibody 3H1 elicits a specific immune response to a

CC unique epitope of carcinoembryonic antigen (CEA) that is not present

CC on other members of the CEA family or on normal adult tissues. 3H1

CC can be used as a vaccine to elicit immune responses in patients

CC with advanced CEA-associated disease or, when labeled, to enhance

CC tumour detection in imaging.

SQ Sequence 142 AA;

Query Match

Best Local Similarity 65.0%; Score 662; DB 18; Length 142;
 Pred. No. 1.28e-39;

Matches 96; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

Db 1 mvsatqflllllwfpgksdkmtqspssmyaslgervltlckasqdinglnwfgqp 60

QY 1 MGAPAOILGFLLEFPGRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHWLOEP 60

Db 61 gkspklllyranrldgypsfsgsgqvytlstssleyedmgtyclqdfefpwmfg 120

QY 61 DGTIKRLIYATSSGSGPKRFSGSGSDYSLTISLSEDFVAYCYCLOAYASSPYTFG 120

Db 121 gtlkrlkradaapvtvsifppss 142

QY 121 GTRKLEIKRADAPTVSIFPPSS 142

Search completed: Thu Apr 15 17:59:17 1999

THIS PAGE BLANK (USPTO)

(TM)

Distribution rights by Oxford Molecular Ltd

Output not generated.

Comp:

TABLE default

Dbase 0; Query 0

602357 seqs, 1181590623 bases x 2

Listing first 45 summaries

emb157

genbank110

33:g_b_un 34:g_b_

mean 10.047; Var

ed by analysis o

SUMMARIES

59.7	739	22	12
------	-----	----	----

45 252 57.

ALIGNMENTS

source

CDS

EDFV DY CY CL QY ASSP YTFGGG TKLEIKR"

```

1. .381
/organism="Mus musculus"
/strain="C57BL/6"

```

	gene	/db_xref="taxon:10090"	/cell_line="splen cell hybridoma"
	CDS	/chromosome="6"	/clone="dc4"
		<1..>381	/gene="Igk"
		1..>381	/gene="Igk"
		/codon_start=1	/product="anti-poly(dc) monoclonal antibody kappa light chain"
		/db_xref="PID:g2906074"	/translation="MRAPOIFKFLILFPETRDIDMTQSPSSLSISGRVLTGRCASDIGNSLNWLOQEPDPGTIRKLRIYATISSLDGVPKRFSGRSSSDISLTISLESEFVDYICQLDIASFPTWFGGGTKLEIK"
	sig_peptide	1..60	
	V_region	/gene="Igk"	61..345
	J_segment	/gene="Igk"	346..>381
	CDR3	/gene="Igk"	90 C 89 g 109 t
	QUERY MATCH	Score 341; DB 29; Length 381;	
	Best Local Similarity	94.8%;	Pred. No. 2,62e-267;
	Matches 361; Conservative	0; Mismatches 20; Indels 0; Gaps 0;	
Db	1	ATGAGGGCTCCTCGCACAAATTGTTGGCTTCTGTGCCTTGTTCCAGGTACCAAGTCAGT	60
Oy	1	ATGGGGGCCCTCGTCAAAATCTTGGGTTCTGTGCTCTGTTCCAGGTACCAAGTCAGT	60
Db	61	GACATCCAGATGACCACATCTCCATCTCTATCTGCTCTGCGAGAAGAGTCAGT	120
Oy	61	GACATCCAGATGACCACATCTCCATCTCTATCTGCTCTGCGAGAAGAGTCAGT	120
Db	121	CTCACTTTCGGGGCAGTCAGACACTTGGTAATAGCTTAAGTGGCTTCAGCAGAACCA	180
Oy	121	CTCACTTTCGGGGCAGTCAGACACTTGGTAATAGCTTAAGTGGCTTCAGCAGAACCA	180
Db	181	GATGAACATATAAAGCGCTGATCTACGCCCATCCAGTAGTTAGTTGTCGTCGCCCAA	240
Oy	181	GATGAACATATAAAGCGCTGATCTACGCCCATCCAGTAGTTAGTTGTCGTCGCCCAA	240
Db	241	AGGTTCACTGCGCAGTAGTCTGCGTCAATATTTCTCCACCATCAGACGCTTGAAGT	300
Oy	241	AGGTTCACTGCGCAGTAGTCTGCGTCAATATTTCTCCACCATCAGACGCTTGAAGT	300
Db	301	GAAATTTTGTAGACTATTACTGCTCTACAATATGCAAGTTTTCCGTGACGTTGGTGA	360
Oy	301	GAAATTTTGTAGACTATTACTGCTCTACAATATGCTAGTATTTCCGTGACGTTGGAGG	360
Db	361	GGACACCAAGCTGGAATCAAA	381
Oy	361	GGGACCAAGCTGGAATATAAA	381
RESULT	4	AF045510	381 bp mRNA ROD 28-FEB-1998
LOCUS		Mus musculus	6c9 monoclonal antibody kappa light chain variable region, (Igk) mRNA, partial cds.
DEFINITION		AF045510	92906103
ACCESSION		NID	house mouse.
KEYWORDS		SOURCE	Mus musculus
ORGANISM			Euxaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			1 (bases 1 to 381)
AUTHORS			O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollari, B.D.
TITLE			Anti-DNA antibodies of normal mice immunized with poly(DC) are structurally similar to natural autoantibodies
JOURNAL			Unpublished

REFERENCE	2 (bases 1 to 381)			
AUTHORS	O'Connor,K.C., Farrell,T.P., Morkawa,A. and Stollar,B.D.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA			
FEATURES	Location/Qualifiers			
source	1..381			
	/organism="Mus musculus"			
	/strain="C57BL/6"			
	/db_xref="taxon:10090"			
	/cell_line="spleen cell hybridoma"			
	/chromosome="6"			
	/clone="6C9"			
gene	1..>381			
	/gene="Igk"			
CDS	1..>381			
	/gene="Igk"			
	/codon_start=1			
	/product="monoclonal antibody kappa light chain"			
	/db_xref="PID:g2906104"			
	/translation="MPAPQIFGLILPFTGRDIOMTSPSSLSISGERVLTORASDIGSSLSMLDEPDGTIKHLIYANSLDSGPKRPFSSRSRSDSLTISLSDSDFDVYCCQYASFPFTSSGIRLEIK"			
sig_peptide	1..60			
	/gene="Igk"			
V_region	61..345			
	/gene="Igk"			
J_segment	346..>381			
	/gene="Igk"			
BASE COUNT	93 a	89 c	87 g	112 t
ORIGIN				
Query Match	77.5%: Score 337; DB 29; Length 381;			
Best Local Similarity	94.2%: Pred. No.9,33e-264;			
Matches	359;	Conservative	0;	Mismatches 22; Indels 0; Gaps 0;
Db	1 ATGAGGGCTCCTGCACAGATTTTGGCTTTGTGTCCTGTGTCAGTACCGAGATGT 60			
Oy	1 ATGGGGGCCCTCGTCACATCTTGCGGTCTTGTTGCTTGTTCACGATCCGAGATGT 60			
Db	61 GACATCCAGATGACCCAGTCATCCTCTTATCTGCTCTCTGGGAGAAAGATCAGT 120			
Oy	61 GACATCCAGATGACCCAGTCATCCTCTTATCTGCTCTCTGGGAGAAAGATCAGT 120			
Db	121 CTCACCTTGGGGGCAAGTCAGACATTTGTCGTGTGTCCTGTGTCAGTACCGAGATGT 180			
Oy	121 CTCACCTTGGGGGCAAGTCAGACATTTGTCGTGTGTCCTGTGTCAGTACCGAGATGT 180			
Db	181 GATGAACTATTTAAACACCTGATCTACGCCACATCCAGATTAGATTGCGTCCCAAA 240			
Oy	181 GATGAACTATTTAAACGCGCTGATCTACGCCACATCCAGATTAGATTGCGTCCCAAA 240			
Db	241 AGGTCAGTGGCAGTAGTGTCGGGTACAGATTATCTCCACCATCAGCAGCGCTGAGTCT 300			
Oy	241 AGGTCAGTGGCAGTAGTGTCGGGTACAGATTATCTCCACCATCAGCAGCGCTGAGTCT 300			
Db	301 GAAGTTTTGTAGACTATTACTGTCTACAATAATGCTAGTTTCCATTACGTTGCGCTCG 360			
Oy	301 GAAGTTTTGTAGACTATTACTGTCTACAATAATGCTAGTTTCCATTACGTTGCGAGGG 360			
Db	361 GGGACCAAGTTGGAATATAA 381			
Oy	361 GGGACCAAGCTGGAAATATAA 381			
RESULT	5			
LOCUS	MMIGVJ1 380 bp RNA ROD 03-FEB-1995			
DEFINITION	M.musculus mRNA for Igk kappa light chain (partial) GI00011.			
ACCESSION	X02177			
MID	g51894			
KEYWORDS	gamma-immunoglobulin; Ig light chain; immunoglobulin; joining region; variable region.			
SOURCE	house mouse.			

ORGANISM	Mus musculus Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 380)
REFERENCE	Darsley,M.J. and Rees,A.R.
AUTHORS	Nucleotide sequences of five anti-Iysozyme monoclonal antibodies
TITLE	EMBO J. 4 (2), 393-398 (1985)
JOURNAL	
MEDLINE	85257466
FEATURES	
source	Location/Qualifiers 1..380 /organism="Mus musculus" /db_xref="taxon:10090"
CDS	<1..>380 /codon_start=3 /product="Immunoglobulin g kappa light chain" /db_xref="PID:g663215" /translation="EGFLWFPGMRDIOQTOSPSLSASIGRVSITCRASEISG YLSRLQKPOSTKRIRLYAASTLSDGVPKRRSSRSBGSDVSLTISSEDFADYYCL OYLSPLETFMGTKLELRADAP" 42..325 /product="variable region of Igk kappa light chain" 111..143 /note="hypervariable region CDR1" 189..212 /note="hypervariable region CDR2" 306..332 /note="hypervariable region CDR3" 326..364 /product="joining region of Igk kappa light chain" 365..>380 /product="constant region of Igk kappa light chain"
V-region	
misc_feature	
misc_feature	
misc_feature	
J-segment	
C_region	
BASE COUNT	88 a 73 c 89 g 110 t
ORIGIN	
Query Match	73.6%; Score 320; DB 29; Length 380;
Best Local Similarity	92.1%; Pred. No.1,13e+24;
Matches 350; Conservative	0; Mismatches 30; Indels 0; Gaps 0;
Db	1 TTTTGCGCTTCGTGGTCGTGCATCCAGGTACCATGTGCATCCAGTAGCCCCAGT 60 Oy 20 TTCTTGCGGTCTCTGTGGCTCTGTGCCAGGTACCAGATGTACACTCCAGTAGCCCCAGT 79 Db 61 CTCGATCCTCCTTAATCTGCCCTCTCGGGAAGAAGTCACTCACCTTGTGCGGCAAGTC 120 Oy - 80 CTCCATCCTCCTTAATCTGCCCTCTCGGGAAGAAGTCACTCACCTTGTGCGGCAAGTC 139 121 AGGAATTAGTCGTACTTAAGCTGGCTTCAGACAATAAACCAGATGGAATTAACGCC 180 Oy 140 AGGACATTGGTATTAACCTTAACCTTGGCTTCAGACAATAAACCAGATGGAATTAACGCC 199 Db 181 TGATCTACGCGCAGCATCACTTAAGATTCGTGGGTCCCAAAGAGTTCAGTGGCAGTAGGT 240 Oy 200 TGATCTACGCGCAGCATCACTTAAGATTCGTGGGTCCCAAAGAGTTCAGTGGCAGTAGGT 259 Db 241 CTGGGTCAGATTATTCCTCACACATCAGCAGCCTTGAAGATTTTGCAGACTATT 300 Oy 260 CTGGGTCAGATTATTCCTCACACATCAGCAGCCTTGAAGATTTTGCAGACTATT 319 Db 301 ACTGCTACAAATATCTTAAGTATCCGGCTCAGGTTGGGTGTGGGACCAAGCTGGAGCTGA 360 Oy 320 ACTGCTACAAATATCTTAAGTATCCGGCTCAGGTTGGGTGTGGGACCAAGCTGGAGCTGA 379 Db 361 AAGGGCTGATGCTGCACCA 380 Oy 380 AACGGGCTGATGCTGCACCA 399
RESULT	6 MMIGVVJZ 381 bp RNA ROD 03-FEB-1995
LOCUS	
DEFINITION	M.musculus mRNA for Igg kappa light chain (partial) GIloop 2.
ACCESSION	X02178
ID	g51899

KEYWORDS	gamma-immunoglobulin; Ig light chain; immunoglobulin; joining region; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphae; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 381)
TITLE	Datslyk,M.J. and Rees,A.R.
JOURNAL	Nucleotide sequences of five anti-lysozyme monoclonal antibodies
MEDLINE	EMBO J. 4 (2), 393-398 (1985)
FEATURES	85257466
Source	Location/Qualifiers
CDS	1..381
	/organism="Mus musculus"
	/db_xref="taxon:10090"
	<1..>381
	/codon_start=1
	/product="immunoglobulin G kappa light chain"
	/db_xref="PID:g663216"
	/translation="VEGFLLMPEPTGRCDIQMTQSPSSASLGERYSLTCARASQEISGYLSWLQKPDGRTIKRLIYAATSLDSCVPRFSGRSGSDSYLTISSEDEPADYYCLOYVSYPLTFEGAGKLEKRNADAP"
	43..326
	/product="variable region of IgG kappa light chain"
	112..144
	/note="hypervariable region CDRI"
	190..213
	/note="hypervariable region CDR2"
	307..333
	/note="hypervariable region CDR3"
	327..365
	/product="joining region of IgG kappa light chain"
	366..>381
	/product="constant region of IgG kappa light chain"
BASE COUNT	90 a 92 c 89 g 110 t
ORIGIN	
Query Match	72.2%; Score 314; DB 29; Length 381;
Best Local Similarity	91.3%; Pred. No. 2,35e-243;
Matches	347; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Db	2 TTTTGGCTTCTGTGCTGTGCTGCTTCCAGGTACAGATGTGACATCCAGATGACCCAGT 61
QY	20 TTTCTGGCTTCTGTGCTGTGCTTCCAGGTACAGATGTGACATCCAGATGACCCAGT 79
Db	62 CTCATCTCTCTTATCTGCCCCCTCTGGAGAAAGATGATGATCTACTTGTGGGCAATC 121
QY	80 CTCATCTCTCTTATCTGCCCCCTCTGGAGAAAGATGATGATCTACTTGTGGGCAATC 139
Db	122 AAGAAATAGTGTACTTAAAGTGGCTTCAGCAAAACCGATGAGAACTTAAAGCC 181
QY	140 AGGACATTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 199
Db	182 TGATCTACGCGCATCCACTTAAATTCCTGCTGCCAAAAAGGTCAAGTGGCAGAGT 241
QY	200 TGATCTACGCGCATCCACTTAAATTCCTGCTGCCAAAAAGGTCAAGTGGCAGAGT 259
Db	242 CTGGGTGAGATTATTTCTCTACCATCAGACACCTTGAATCTGAAGATTTTCAACATAT 301
QY	260 CTGGGTGAGATTATTTCTCTACCATCAGACACCTTGAATCTGAAGATTTTCAACATAT 319
Db	302 ATTGCTACCAATATCTTATGTTATCCGGTCAGGTCGGGTGGGACCAAGCTGGAGCTGA 361
QY	320 ACTGTCTCAATATAGTAGTGTCTCCGTAACAGGTTGGAGGGGGGACCAAGCTGGAATAA 379
Db	362 AACGGCTGATGCTGCACCA 381
QY	380 AACGGCTGATGCTGCACCA 399
RESULT	7
LOCUS	MUSIGKCM 383 bp mRNA ROD 15-MAR-1989

SEGMENT	1 of 3
SOURCE	Mus musculus myeloma DNA.
ORGANISM	Mus musculus
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 684) Seidman,J.G., Max,E.E. and Leder,P.
TITLE	A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation
JOURNAL	Nature 280 (5721), 370-375 (1979)
MEDLINE	79221900
REFERENCE	2 (sites)
AUTHORS	Queen,C. and Baltimore,D.
TITLE	Immunoglobulin gene transcription is activated by downstream sequence elements
JOURNAL	Cell 33 (3), 741-748 (1983)
MEDLINE	83259260
COMMENT	[3] sites; comment. this sequence is a productively rearranged kappa ig from myeloma mopc41. the conflicts noted in the sites table refer to the published differences between the germline and active genes. they are probably typographical errors since [1] says that no somatic mutation has occurred after recombination. j.g. seidman (personal communication) said that the published germline sequence is correct <musikvc>. [2] finds that deletion of 1.3kb 5' to the constant region exon results in a lowered rate of transcription and an altering of the site of transcription initiation. the deletion moves transcription initiation from approximately 30 bp 5' to the initiation codon to about 20 bp 5'. for part of the vk41 constant gene and part of the 3' flank see <musikac2> and <musikajc3> respectively. for the germline joining j1 region see <musikjcz>. for other rearranged kappa genes see loci beginning <musikga>, and for germline kappa variable genes see loci beginning <musikgv>. in the sites table cdr-complementarity determining region and fr-framework region. Location/Qualifiers 1. .684 /organism="Mus musculus" /db_xref="taxon:10090" /cell_line="MOPC41" /tissue_type="myeloma" <119. .173 /gene="Igk" /number=1 sig_peptide join(119. .173,302. .312) intron /partial /gene="Igk" 174. .301 /gene="Igk" /number=1 302. .634 /gene="Igk" /number=2 596. .597 /gene="Igk" misc_recomb /organism="Mus musculus" BASE COUNT 164 a 156 c 147 g 217 t ORIGIN 110bp 5' to HinfI site 4bp 5' to exon 1, chromosome 6. Query Match 71.3%; Score 310; DB 29; Length 684; Best Local Similarity 96.1%; Pred. No. 8, 21e-240; Matches 323; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db	300 AGTACAGATGTGACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGG 359 48 AGGTACAGATGTGACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGG 107
Db	360 AGAAGAGTACGTCTACTGTGGGGCAGTACAGAGCATGTGTACTACTTAACTGGCT 419 108 ACAAGAGTACGTCTACTGTGGGGCAGTACAGAGCATGTGTACTACTTAACTGGCT 167
Db	420 TCACAGAGAACCCAGATGACATTTAAAGCGCTGATCTACGCGACATCCAGTTAGATTC 479

```

|||||
QY 168 TCACAGGAACACGATGTAACATATTAACGCTATCTACCCACATCCAGTTAGTTC 227
Db 480 TGGTGTCCCCAAAAGTTCACTGCGAGTAGTCTGGGTCAATATTCTCTCCACATCAG 539
QY 228 TGGTGTCCCCAAAAGTTCACTGCGAGTAGTCTGGGTCAATATTCTCTCCACATCAG 287
Db 540 CAGCCTTGAGCTGAAGATTTGTAGACTATTACTAGTACAAATGCTAGTCCGCTG 599
QY 288 CAGCTTGAGCTGAAGATTTGTAGACTATTACTAGTACAAATGCTAGTCCGCTG 347
Db 600 GAGCCTTGAGCTGAAGATTTGTAGACTATTACTAGTACAAATGCTAGTCCGCTG 635
QY 348 CAGCTTGAGCTGAAGATTTGTAGACTATTACTAGTACAAATGCTAGTCCGCTG 383

RESULT 9
LOCUS AB016620 405 bp mRNA ROD 06-AUG-1998
DEFINITION Mus musculus mRNA for Immunoglobulin light chain variable region, partial cds.
ACCESSION AB016620
KEYWORDS Immunoglobulin light chain variable region.
SOURCE Mus musculus cell_line:FU-MK-1 hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euteria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Arakawa,F., Yamamoto,T., Kanda,H., Watanabe,T. and Kuroki,M.
TITLE Cloning and sequencing of cDNAs encoding the variable domains of monoclonal antibody FU-MK-1 specific for a transmembrane carcinoma-associated antigen, and construction of a mouse/human chimeric antibody
JOURNAL Unpublished (1998)
REFERENCE 2 (bases 1 to 405)
AUTHORS Arakawa,F.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1998) to the DDBJ/EMBL/Genbank databases. Fumiko Arakawa, School of Medicine, Fukuoka University, First Department of Biochemistry, 7-45-1 Nanakuma, Jonan-ku, Fukuoka, Fukuoka 814-80, Japan (E-mail:farakawa@sat.fukuoka-u.ac.jp, Tel:092-801-1011(ex.3246), Fax:092-801-3600)
FEATURES
source
1..405
/organism="Mus musculus"
/note="The hybridoma producing anti-GA733-2 monoclonal antibody"
/db_xref="taxon:10090"
/cell_line="FU-MK-1 hybridoma"
1..43
/note="PCR primer region"
primer_bind
1..392
11..392
11..392
/codon_start=1
/product="Immunoglobulin light chain variable region"
/db_xref="PID:d1033042"
/db_xref="PID:g3395671"
/translation="MRAPAQILGLIMFPGICRDIKMTGSPSSLSLGERVLTGR ASQETISGLSMLOQPDGTVKRLIYASTHSQVPRFSGSRGSDSYSLTISLESDD FADYVCLQYASDPWTFEGGKLEIK"
sig_peptide
11..70
primer_bind
393..405
/note="PCR primer region"
intron
393..405
BASE COUNT 98 a 100 c 97 g 110 t
ORIGIN
Query Match 71.0%; Score 309; DB 29; Length 405;
Best Local Similarity 90.3%; Pred.No.6,31e-239;
Matches 346; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Db 11 ATGAGGCCCCGCTCAGATCTTGGCTTCTGTGCTCTGTTCCAGTATTAGATGT 70
|||||

```

```

QY 1 ATGGGGCCCCCTGCTCAGATCTTGGGTTCTGTGCTTGTTCAGGATACAGATGT 60
Db 71 GACATCAAGATGACCCAGTCGCCATCTCTTATCTGCTCTGGAGAAAGTCACT 130
QY 61 GACATCCAGATGACCCAGTCGCCATCTCTTATCTGCTCTGGAGAAAGTCACT 120
Db 131 CTCAGTTGGGGGCAAGTCAGGAATTAAGTGTACTTAAGTCTGCTGCAAAAAACA 190
QY 121 CTCAGTTGGGGGCAAGTCAGGAATTAAGTGTACTTAAGTCTGCTGCAAAAAACA 180
Db 191 GATGAACCTGTTAAACCCCTGATCTACGCCGATCCACTTACATTCTGGTCCAAA 250
QY 181 GATGAACCTGTTAAACCCCTGATCTACGCCGATCCACTTACATTCTGGTCCAAA 240
Db 251 AGTTCACTGAGTACAGTCTGGTCTGAGTCTGCTACACTTCTCTACCATCAGACGCTTGA 310
QY 241 AGTTCACTGAGTACAGTCTGGTCTGAGTCTGCTACACTTCTCTACCATCAGACGCTTGA 300
Db 311 GAGCATTTTGACAGCTATTACTGCTACAGTATGCTATGCTGATCCGTGGAGTCCG 370
QY 301 GAGCATTTTGACAGCTATTACTGCTACAGTATGCTATGCTGATCCGTGGAGG 360
Db 371 GGCACCAAGCTGGAATCAACG 393
QY 361 GGCACCAAGCTGGAATCAACG 383

RESULT 10
LOCUS NMIGK7 685 bp DNA ROD 21-NOV-1994
DEFINITION Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).
ACCESSION U00808 J00565
KEYWORDS 952134
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euteria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 685)
AUTHORS Seidman,J.G., Max,E.E. and Leder,P.
TITLE A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation
JOURNAL Nature 280 (5721), 370-375 (1979)
MEDLINE 79221900
COMMENT KST MMU. IGHAP.MOPC41.
FEATURES
source
1..685
/organism="Mus musculus"
/db_xref="taxon:10090"
sig_peptide
120..173
join(120..173,302..>637)
CDS
120..173
/codon_start=1
/product="Immunoglobulin kappa"
/db_xref="PID:g577074"
/translation="MDMRAPAQIFGLLIFPGTRDIDMTGSPSSLSLGERVLT CRPSDQISGLSMLOQPDGTVKRLIYASTHSQVPRFSGSRGSDSYSLTISLES FADYVCLQYASDPWTFEGGKLEIK"
302..637
exon
302..637
BASE COUNT 164 a 158 c 146 g 217 t
ORIGIN
Query Match 70.8%; Score 308; DB 29; Length 685;
Best Local Similarity 95.8%; Pred.No.4,85e-238;
Matches 322; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Db 301 AGTACCAAGATGTACATCCAGATGACCAAGTCTCCATCTCTTATCTGCTGCG 360
QY 48 AGTACCAAGATGTACATCCAGATGACCAAGTCTCCATCTCTTATCTGCTGCG 107
Db 361 AGAAGAGTCACTGCTGCTGCGCAAGTCAAGCAATGTGTAGTCTTAACCTGGCT 420
QY 108 ACAAGAGTCACTGCTGCTGCGCAAGTCAAGCAATGTGTAGTCTTAACCTGGCT 167

```

Db 421 TCACGAGAACGATGGAATTAAGCCCTGATCTACGCCACATCCAGTTAGATTC 480
|||||
Qy 168 TCACGAGAACGATGGAATTAAGCCCTGATCTACGCCACATCCAGTTAGATTC 227
Db 481 TGGTGTCCCAAAAGGTTAGTGCAGTAGTGGTGCAGTATGATCTCTCCATCAG 540
|||||
Qy 228 TGGTGTCCCAAAAGGTTAGTGCAGTAGTGGTGCAGTATGATCTCTCCATCAG 287
Db 541 CAGCCTTGAGTCTGAAGATTTGTAGACTATTAATGCTTACAAATAGTATTCCTG 600
|||||
Qy 288 CAGCCTTGAGTCTGAAGATTTGTAGACTATTAATGCTTACAAATAGTATTCCTG 347
Db 601 GAGCTCGGTGAGGAGCAGCAGCTGGAATCAACG 636
|||||
Qy 348 CAGCTTCGGAGGGGGAGCAGCTGGAATCAACG 383

RESULT 11
LOCUS MUSX 324 bp mRNA ROD 07-JAN-1997
DEFINITION Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody
ACCESSION L48667
NID 91050293
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE 1 (bases 1 to 324)
AUTHORS Mloch, M.K., Alexander, A.L., Phippen, A.M., Pisetsky, D.S. and Gillespie, G.S.
TITLE Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-1pr mice and lupus mice with nephritis
JOURNAL Eur. J. Immunol. 26 (9), 2225-2233 (1996)
MEDLINE 96409289
FEATURES
Location/Qualifiers
source 1..324
/organism="Mus musculus"
/strain="C3H/HeJ-1pr"
/db_xref="taxon:10090"
/cell_line="C3H/F2-15"
/cell_type="hybridoma"
/tissue_type="spleen"
BASE COUNT 83 a 76 c 77 g 87 t 1 others
ORIGIN
Query Match 69.9%; Score 304; DB 28; Length 324;
Best Local Similarity 96.9%; Pred. No. 1,69e-234;
Matches 313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 361 GGGACCAAGCTGGAAATTAACG 383
|||||

RESULT 12
LOCUS AR007981 739 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 5 from patent US 5753204.
ACCESSION AR007981
NID 93967090
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 739)
AUTHORS Huston, J.S., Huston, L.L., Ring, D.B. and Oppermann, H.
TITLE Biosynthetic binding proteins for immunotargeting
JOURNAL Patent: US 5753204-A 5 19-MAY-1998;
FEATURES
Location/Qualifiers
source 1..739
/organism="unknown"
BASE COUNT 188 a 177 c 181 g 193 t
ORIGIN
Query Match 69.7%; Score 303; DB 22; Length 739;
Best Local Similarity 95.2%; Pred. No. 1.29e-233;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 395 GATCCATATCCAGATGACCCAGTCCATCCCTCTATCTGCTCTGGAGAAAGAG 454
|||||
Qy 56 GATGTACATCCAGATGACCCAGTCCATCCCTCTATCTGCTCTGGAGAAAGAG 115
Db 455 TCAGTCTCACTTGTCCGGCAAGTCAGACATTGGTAATAGCTTACCTGCTTCAGCAG 514
|||||
Qy 116 TCAGTCTCACTTGTCCGGCAAGTCAGACATTGGTAATAGCTTACCTGCTTCAGCAG 175
Db 515 AACCAATGGAATATTAACGCTCATCTAGCCACATCCATTAATGATTCGGTGTCC 574
|||||
Qy 176 AACCAATGGAATATTAACGCTCATCTAGCCACATCCATTAATGATTCGGTGTCC 235
Db 575 CCAAAAGTTCAGTGGCAGTCGCTGGGTGAGATTAATCTCCACATCAGTAGCTTG 634
|||||
Qy 236 CCAAAAGTTCAGTGGCAGTCGCTGGGTGAGATTAATCTCCACATCAGTAGCTTG 295
Db 635 AGCTGAAGATTTGTAGTCTATTACTGTCTACAAATGCTATTTTCGTACACGTTGC 694
|||||
Qy 296 AGCTGAAGATTTGTAGTCTATTACTGTCTACAAATGCTATTTTCGTACACGTTGC 355
Db 695 GAGGGGGACCAACTGGGAATTAACGGGCTGAT 729
|||||
Qy 356 GAGGGGGACCAACTGGGAATTAACGGGCTGAT 390
|||||

RESULT 13
LOCUS I23446 739 bp DNA PAT 09-JUL-1996
DEFINITION Sequence 5 from patent US 5534254.
ACCESSION I23446
NID 91603316
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 739)
AUTHORS Huston, J.S., Huston, L.L., Ring, D.B. and Oppermann, H.
TITLE Biosynthetic binding proteins for immunotargeting
JOURNAL Patent: US 5534254-A 5 09-JUL-1996;
FEATURES
Location/Qualifiers
source 1..739
/organism="unknown"
BASE COUNT 188 a 177 c 181 g 193 t
ORIGIN
Query Match 69.7%; Score 303; DB 22; Length 739;
Best Local Similarity 95.2%; Pred. No. 1.29e-233;






Sun Apr 18 10:25:06 1999

US-08-836-455-1.rge

Page 9

Search completed: Sat Apr 17 14:27:52 1999
Job time : 1710 secs.

THIS PAGE BLANK (USPTO)

Release 3.1A John F. Collins, Biocomputing Research Unit
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

```

Mpsrch_un n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Apr 17 14:55:39 1999; Maspar time 751.66 Seconds
Maspar output not generated. 1449.353 Million cell updates/sec

```

```

Title: >US-08-836-455-3
Description: (1-461) from US0836455.seq
Perfect Score: 461
N.A. Sequence:
Comp: 1 ATGGATGTCAGCTGGGCTCT.....CTGTCCCTCGAAGCTTGGG 461
TACCTTACGTCGACCCAGAA.....GACCAGGGACCTCTGAAACC

```

Scoring table: TABLE default

```
Nmatch      STD : Dbase 0; Query 0
```

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

```
Database:
    emb157
    1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
    7:em_com 8:em_for 9:em_ovr 10:em_pat 11:em_ph 12:em_pl
    13:em_to 14:em_un 15:em_y1
    genbank110
```

```

16:gd_ba1 17:gd_ba2 18:gd_hcy 19:gd_in 20:gd_om 21:gd_ov
22:gd_pat 23:gd_ph 24:gd_p11 25:gd_p12 26:gd_prl
27:gd_pr2 28:gd_pr3 29:gd_ro 30:gd_st 31:gd_sts 32:gd_sy
33:gd_un 34:gd_vl

```

stics: Mean 10.230; Variance 5.449; scale 1.878

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	314	68.1	458	22	109199	Sequence 38 from Paten	2.71e-216
2	314	68.1	458	29	MUSICHXM	Mouse Ig rearranged H-	2.71e-216
3	314	68.1	458	22	105921	Sequence 37 from Paten	2.71e-216
4	314	68.1	458	22	108811	Sequence 12 from Paten	2.71e-216
5	303	65.7	902	32	XXU49832	Synthetic single chain	1.32e-2076
6	289	62.5	351	29	MMLB1HEV	M.musculus DNA for IGE	1.46e-196
7	288	62.5	454	29	MMAIDHCH	M.musculus mRNA for an	8.94e-166
8	285	61.8	357	29	MUSY	Mus musculus (cell lin	2.06e-153
9	279	60.5	335	29	MAMD47C	M.musculus mRNA for re	1.09e-188
10	277	60.1	358	29	MAMD10C	M.musculus mRNA for re	4.10e-187
11	276	59.9	352	29	MNMD50C	M.musculus mRNA for re	2.51e-186
12	275	59.7	415	29	AF045892	Mus musculus Ig2a cha	1.54e-185
13	275	59.7	525	29	MUSIHALPA	Mus musculus Ig2a cha	1.54e-185

15	275	59.7	540.22	A13735	Variable region of a m	1.54e-185
14	273	59.2	588.22	A23165	Artificial construct c	5.75e-184
16	273	59.2	588.29	MUSIGGVAV	Mus. musculus IgG chain	5.75e-184
17	271	58.8	490.29	MUSIG4C11A	Mus mus anti-1dotype imm	2.15e-182
18	270	58.6	484.29	MUSIG4C11	Mouse IgH chain mRNA,	1.32e-181
19	268	58.1	417.29	AF045501	Mus musculus 6E6 monoc	4.91e-180
20	268	58.1	1500.29	MMAM692	M. musculus mRNA for mo	4.91e-180
21	267	57.9	474.29	MMU39888	Mus musculus anti-glyc	3.00e-179
22	266	57.9	477.29	MUSVROG	Mus musculus anti-1gyc	1.83e-178
23	265	57.5	462.29	MUSIGKGLS	Mouse IgMk rearranged	1.12e-177
24	265	57.5	1581.29	MUSIGHC1A	M. musculus mRNA for mo	1.12e-177
25	264	57.3	1544.29	MUSIGB11A	Mouse mRNA for immunog	6.83e-177
26	263	57.0	420.22	AR015963	Sequence 5 from patent	4.16e-176
27	263	57.0	420.22	AR000013	Sequence 5 from patent	4.16e-176
28	263	57.0	690.29	MMU28968	Mus musculus Mab9y ant	4.16e-176
29	263	57.0	9209.22	AR015961	Sequence 2 from patent	4.16e-176
30	263	57.0	9209.22	AR000007	Sequence 3 from patent	4.16e-176
31	262	56.8	360.29	MUSAL	Mus musculus (cell lin	2.54e-175
32	261	56.6	411.29	A51507	Sequence 9 from Patent	1.55e-174
33	261	56.6	411.29	MMU5946	Mus musculus mRNA for	1.55e-174
34	261	56.6	422.22	AR013881	Sequence 77 from paten	1.55e-174
35	261	56.6	462.29	MUSIGKICP	Mouse IgMk rearranged	1.55e-174
36	260	56.4	508.29	MUSIGGF3A	Mouse anti-1dotype imm	9.45e-174
37	259	56.2	437.29	MUSIGF3A	Mouse Ig active H-chain	5.76e-173
38	258	56.0	450.22	A07953	Artificial sequence fo	3.51e-172
39	258	56.0	1546.29	MMTWIIGH	M. musculus rearranged	3.51e-172
40	258	56.0	1579.29	MMIG66H	Mouse mRNA for anti-hp	3.51e-172
41	257	55.7	483.29	MMU39899	Mus musculus anti-glyc	2.14e-171
42	256	55.5	302.29	MMIGSCVRI	M. musculus immunoglob	1.30e-170
43	256	55.5	305.29	MMIGCVRE	M. musculus immunoglob	1.30e-170
44	255	55.3	414.29	MUSIGFTH	Mouse Ig active alpha	7.93e-170
45	255	55.3	536.29	MMIGW65B	M. musculus W655 immuno	7.93e-170

ALIGNMENTS

	RESULT	1			PAT	14-NOV-1994
LOCUS	Sequence	38	from Patent WO 8900999.			
DEFINITION	Sequence	38	from Patent WO 8900999.			
ACCESSION	109199					
NID	g588126					
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 458)					
TITLE	Robinson,R.R., Liu,A.Y., Horwitz,A.H., Wall,R. and Better,M. MODULAR ASSEMBLY OF ANTIBODY GENES, ANTIBODIES PREPARED THEREBY AND USE					
JOURNAL	Patent: WO 8900999-A 38 09-FEB-1989;					
FEATURES	Location/Qualifiers					
source	1..458					
BASE COUNT	113 a 120 c 112 g 113 t					
ORIGIN	"organism="unknown"					
Query Match	68.1%; Score 314; DB 22; Length 458;					
Best Local Similarity	94.6%; Pred.No.2,71e-216;					
Matches	333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;					
Db	39 ATGGAGTACGACGAGATCTTTCTCTTCCTCCTGTGCAGTACTACAGGTGTCACATCCCG 98					
OY	1 AWMGATGACGCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCAATATACAGGTGTCACATCCCG 60					
Db	99 GCCTATCTACACGACAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCCTCAGTAGAATGTTC 158					
OY	61 GCTTATCTACACGACAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCCTCAGTAGAATGTTC 120					
Db	159 TGCAGGCTTGGCTACACATTATTCAGGTACAATATGACACTGGGTAAACGACACACT 218					
OY	121 TGCAAGCTTCTGGCTACACATTGACCAGTTACAAATATGACACTGGGTAAACGACACACT 180					
Db	219 AGACAGGCCCTGGAGATGGAGCTATTATATCAGGAATAAGATGATCTCTCACAT 278					

|||||
OY 181 GGACAGGGGCTGGATGATTTGGAAATATTTTCCGGGAAAGGATGATCTTACTACAT 240
Db 279 CAGAAGTTCAAGGCAAGGCCACACTGACTGTAGACAAATCTCCAGACAGCCTACATG 338
OY 241 CAGAAGTTTAAAGGCAAGGCCCTCATTTAGTGCAGACATCTCCAGACAGCCTACATG 300
Db 339 CAGCTCAGAGCCTGACATCTGAGACTGTGGGCTATTGTCGCAAG 390
OY 301 CAGATCAGACGCTGACATCTGAGACTGTGGCTATTGTCGCAAG 352
RESULT 2
LOCUS MUSIGHX 458 bp mRNA ROD 26-MAR-1994
DEFINITION Mouse Ig rearranged H-chain V-region mRNA VJ1.
ACCESSION M7953
NID 9196223
KEYWORDS C-region; V-region; Immunoglobulin heavy chain; processed gene.
ORGANISM Mus musculus
MUS musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphia; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 458)
AUTHORS Liu,A.Y., Robinson,R.R., Murray,E.D.Jr., Ledbetter,J.A.,
Hellstrom,I. and Hellstrom,K.E.
TITLE Production of a mouse-human chimeric monoclonal antibody to CD20
JOURNAL with potent Fe-dependent biologic activity
MEDLINE J. Immunol. 139, 3521-3526 (1987)
COMMENT 8806045
FEATURES
SOURCE A.Y.Liu, 02-FEB-1987.
Location/Qualifiers
1..458
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="2H7"
39..>458
/note="VJ1-region"
/codon_start=1
/product="immunoglobulin heavy chain"
/db_xref="PID:g196224"
/translation="MGFSRIFPLISVTGHSOAYLOOGSAELVPRGASYKMSCKAS
GTFETSYNMHVKNQTPROGLEMLGAIVYNGNDSTYNGKFKALITLYDKSSITAYMOL
SSTISDSAVYFCARVITYNSYTFDWMGCTVTVS"
410..411
/note="V-region end/31-region start"
/organism="Mus musculus"
BASE COUNT 113 a 121 c 111 g 113 t
ORIGIN
Query Match 68.1%; Score 314; DB 29; Length 458;
Best Local Similarity 94.6%; Pred. No. 2,71e-216;
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 241 CAGAAGTTTAAAGGCAAGGCCCTCATTTGACTGCAGACATCTCCAGACAGCCTACATG 300
Db 339 CAGCTCAGACGCTGACATCTGAGACTGTGGGCTATTGTCGCAAG 390
OY 301 CAGATCAGACGCTGACATCTGAGACTGTGGCTATTGTCGCAAG 352
RESULT 3
LOCUS 105921 458 bp PAT 14-NOV-1994
DEFINITION Sequence 37 from Patent EP 0274394.
ACCESSION 105921
NID 9590876
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 458)
AUTHORS Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and
Ledbetter,J.A.
TITLE Chimeric antibody with specificity to human B cell surface antigen
JOURNAL Patent: EP 0274394-A2 37 13-JUL-1988;
FEATURES Location/Qualifiers
1..458
/organism="unknown"
BASE COUNT 113 a 120 c 112 g 113 t
ORIGIN
Query Match 68.1%; Score 314; DB 22; Length 458;
Best Local Similarity 94.6%; Pred. No. 2,71e-216;
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 39 ATGGATTTCAGAGGATCTTCTCTCTCCCTGTCAGTAACAGAGCTGTCACCTCCAG 98
OY 1 ATGGATGACAGCTGGGCTCTTCTCTCTCTCTCTCTCAATTAACAGAGGTCACCTCCAG 60
Db 99 GCTTATCTACAGACAGCTGTGGGCTGAGCTGTGAGGCTCAGTGAAGATGTC 158
OY 61 GCTTATCTACAGACAGCTGTGGGCTGAGCTGTGAGGCTCAGTGAAGATGTC 120
Db 159 TGCAGGCTTCTGGCTACACATTTACAGTTACAAATATGACTGGTTAAAGCAGACCT 218
OY 121 TGCAGGCTTCTGGCTACACATTTACAGTTACAAATATGACTGGTTAAAGCAGACCT 180
Db 219 AGACAGGGCCCTGGAATGATTTGAGCTATTATCCAGAAATGSGTATCTCTCAAT 278
OY 181 GGACAGGGCCTGGGAATGATTTGAGCTATTATCCAGAAATGSGTATCTCTCAAT 240
Db 279 CAGAAGTTCAAGGCAAGGCCACACTGACTGTAGACAAATCTCCAGACAGCCTACATG 338
OY 241 CAGAAGTTTAAAGGCAAGGCCCTCATTTAGTGCAGACATCTCCAGACAGCCTACATG 300
Db 339 CAGCTCAGACGCTGACATCTGAGACTGTGGGCTATTGTCGCAAG 390
OY 301 CAGATCAGACGCTGACATCTGAGACTGTGGCTATTGTCGCAAG 352
RESULT 4
LOCUS 108811 458 bp PAT 14-NOV-1994
DEFINITION Sequence 12 from Patent WO 8804936.
ACCESSION 108811
NID 9588489
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 458)
AUTHORS Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and
Ledbetter,J.A.
TITLE Patent: WO 8804936-A 12 14-JUL-1988;
FEATURES Location/Qualifiers
1..458
/organism="unknown"
BASE COUNT 113 a 120 c 112 g 113 t

D	b		41	ATGGAATTGATGTGGTCTTTCTCTTCCTCCCTGTAAGTACTGACAGTGTCACACTGTGAG	100
O	y		1	ATGGAAATGAGGTGGGTCTTTCTCTTCCTCCCTGTAATTAACAAGTGTCCACGCCAG	60
D	b		101	GTCGCACTTCACACACTCTTGAGCTGAGCTGGAGCGGCCTGCTCCAGTAGAAGATGTC	160
O	y		61	GCTTATCTAACACAGTCTGGGGCTGAGCTGGTGGAGTCTGGGGCCTCAAGTAAGATGTC	120
D	b		161	TGCAGAAGTCTGTGATATACATTCACAACAGCTAGGTATAACTGGGTGAAGCAGAGCCT	220
O	y		121	TGCAGAGCTTCTGGCTACACATTGACACAGTATCAATATGCACTGGGTAAAGCAGACCT	180
D	b		221	GGACAGGGCGCTGAATGATGATATATTTATTTGATATGATGATATTTAGATAT	280
O	y		181	GGACAGGGCGCTGAATGATGATGATATATTTATTTGATATGATGATATTTAGATAT	240
D	b		281	GAGAAGTTCAGAGGAGGAGCCACACTGACTGATTCAGACACATCTCCAGCAGACCTACATG	340
O	y		241	CAGAGTTTAAAGGCAAGGCCCTCATTTGATGATGACAGACATCTCCAGCAGACCTACATG	300
D	b		341	CACATCAGCAGCCTTACATCTGAGGACTCTGCAATCTATTTCTGCAAGATGGGCTTA	400
O	y		301	CAGATCAGCAGCCTTACATCTGAGGACTCTGCAATCTATTTCTGCAAGATGGGCTTA	360
D	b		401	ATCTTGTGATGAGTACTAGTGGGCTGAAGAACTCAGTACACCCTGCTCCA	461
O	y		361	GAGGTGCTCTGACTGACTGGGCTGAAGAACTCAGTACACCCTGCTCCA	421
R	E	S	7	MALDRCH	354 bp RNA ROD 05-JUN-1993
L	O	C		LOCUS	
D	E	F		DEFINITION	M.musculus mRNA for anti-id mAb 114 heavy chain, variable region.
A	C	C		ACCESSION	X64805
N	I	D		KEYWORDS	anti-idiotypic antibody.
K	E	Y		SOURCE	house mouse.
O	R	G		ORGANISM	Mus musculus
					Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
					Vertebrate; Eutheria; Rodentia; Sciurognathi; Myomorphia; Muridae;
					Murine; Mus.
					1 (bases 1 to 354)
					Zemke,G., Zeder,G., Strittmatter,U., Andersen,E., Kochev,H.P.,
					Queniaux,V.F., Schreiber,M.H. and Van Regenmortel,M.H.
					Anti-cyclosporine monoclonal antibodies and their anti-idiotypic
					counterpart: structure and biological activity
					Mol. Immunol. 29 (3), 343-351 (1992)
					92212306
F	E	A		FEATURES	
				source	Location/Qualifiers
					1..354
					/organism="Mus musculus"
					/strain="BALB/c"
					/db_xref="taxon:10090"
					1..354
					/partial
					/codon_start=1
					/product="anti-id mAb 114 heavy chain, V-region"
					/db_xref="PID:g313232"
					/translation="QATLQDSGAEIIVPSSVSKMSKASGYTFSTNMHWKQTPTROG
					LEWIGAIYPNGDTSYNQKEFGKATLVVDKSSSTAYMQLSLSEDAVFYCARGDYS
					GSIDYMQGTLTVSS"
B	A	S		BASE COUNT	94 a 90 c 89 g 81 t
O	R	I		ORIGIN	
Q	U	E		Query Match	62.5%; Score 288; DB 29; Length 354;
				Best Local Similarity	90.7%; Pred. No. 8,94e-196;
				Matches	321; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
D	b		1	CAGGCTTATACACACAGCTGCGGCTGAGCTGGTAAGCCCTGGCTCTCAAGTGAATG	60
O	y		58	CAGGCTTATACACACAGCTGCGGCTGAGCTGGTAAGCCCTGGCTCTCAAGTGAATG	117
D	b		61	TCTGCAAGGCTTCTGGCTACACATTTACAGTTACCAATATGCACTGGGTAAAGCAGCA	120

QY	118	TCCTGCAGAGCCTTCTGGCTACACATTGACACAGTACCAATATATGCACCTGGGCTAAAGCAGACA	177
Db	121	CCATACAGAGGCGCTGGAAATGATTTGAGCTATTTATTCAGAGAAATGTTGATCTCTCTAC	180
QY	178	CCTGCACAGGCGCTGGAATGATTTGAAATATTTTTCTGGAATATGTTACTTACTTACTAC	237
Db	181	AATCAGAAGTTCAAGGGCAGAGGCCACACCTGACCTGTGACAAATCTCTCCAGCACACCTTAC	240
QY	238	AATCAGAAGTTTAAAGGGCAGAGGCGCTCATTTGACCTGACAGACACATCTCCAGCCACCTTAC	297
Db	241	ATGCAGCTCACACACCTCGACATCTGGAAGACTCTGGCGTATTTCTGTGTCAGAGGGGAT	300
QY	298	ATGCAGATCACACACCTCGACATCTGAGAGACTCTGGCGTATTTCTGTGTCAGAGGGGAT	357
Db	301	TACTCCGCTAGTATATAGACTGTGGGGCCAGAGCCACACCTCTGCACAGTCTCTCA	354
QY	358	TGGGAGGCTGCTGTGACACTCTGGGGGCAAGAGAACCTCAGTACCGCTCTCTCA	411
RESULT	8		
LOCUS	MUSY	357 bp	RNA
DEFINITION	Mus musculus (cell line C3H/Fe-20)	chromosome 12	anti-DNA antibody
ACCESSION	U48668		
NID	91050294		
KEYWORDS	house mouse, Mus musculus		
SOURCE	ORGANISM		
REFERENCE	1 (bases 1 to 357)		
AUTHORS	Wloch,M.K., Alexander,A.L., Pippen,A.M., Pisetsky,D.S. and Gilkeson,G.S.		
TITLE	Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-1pr mice and lupus mice with nephritis		
JOURNAL	Eur. J. Immunol.	26 (9), 2225-2233	(1996)
MEDLINE	96409289		
FEATURES	Location/Qualifiers		
source	1..357		
BASE COUNT	94 a 88 c 89 g 85 t	1 others	
ORIGIN			
Query Match	61.8%; Score 285; DB 29; Length 357;		
Best Local Similarity	91.9%; Pred. No. 2, 0.06-1.93;		
Matches	328; Conservative 0; Mismatches 26; Indels 3; Gaps 1;		
Db	1	CAGGCTAATATACAGCAGTCTGGGCGCTGAGCTGTGAGGCGCTGAGGCGCTCAGTGAAGATG	60
QY	58	CAGGCTAATATACAGCAGTCTGGGCGCTGAGCTGTGAGCTGTGAGGCGCTCAGTGAAGATG	117
Db	61	TCCGCAAGGCTTCTGGCTACACATTACACAGTTCACAAATATGCATCTGGGTAAAGCAGACA	120
QY	118	TCCGCAAGGCTTCTGGCTACACATTGACCAAGTTCACAAATATGCATCTGGGTAAAGCAGACA	177
Db	121	CCATACAGAGGCGCTGGAATGATTTGAGCTATTTATTCAGAGAAATGTTGATCTCTCTAC	180
QY	178	CCATACAGAGGCGCTGGAATGATTTGGAATATTTTTCTGGAATATGTTGATCTCTCTAC	237
Db	181	AATCAGAAGTTCAAGGGCAGAGGCCACACCTGACCTGTGACAAATCTCTCCAGCACACCTTAC	240
QY	238	AATCAGAAGTTTAAAGGGCAGAGGCGCTCATTTGACCTGACAGACACATCTCCAGCCACCTTAC	297
Db	241	ATGCAGCTCACACACCTCGACATCTGGAAGACTCTGGCGTATTTCTGTGTCAGAGAGCTTAT	300
QY	298	ATGCAGATCACACACCTCGACATCTGGAAGACTCTGGCGTATTTCTGTGTCAGAGAGGAT	357
Db	301	TACTCCGCTAGTATATAGACTGTGGGGCCAGAGCCACACCTCTGCACAGTCTCTCA	354
QY	358	TGGGAGGCTGCTGTGACACTCTGGGGGCAAGAGAACCTCAGTACCGCTCTCTCA	411

RESULT	9	MMMD47C	355 bp	RNA	ROD	20-DEC-1996
LOCUS		M.musculus mRNA for rearranged Ig heavy chain V region (J588				
DEFINITION		family; 129Md.4/c).				
ACCESSION		Z73342				
NID		g1322170				
KEYWORDS		antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.				
SOURCE		house mouse.				
ORGANISM		Mus musculus				
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE		1 (bases 1 to 355)				
JOURNAL		Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Gilfillan,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Maki,T.W. and Rajewsky,K. Somatic Hypermutation occurs in B cells of Tdt, CD23, IL-4, Igd and CD30 deficient mouse mutants				
REFERENCE		Unpublished				
AUTHORS		2 (bases 1 to 355)				
TITLE		Mueller,W.				
JOURNAL		Direct Submission				
REFERENCE		Submitted (14-MAY-1996) Mueller W., Institute for Genetics at the University of Cologne, Weyerling 121, Cologne 50931, Germany				
AUTHORS		3 (bases 1 to 355)				
TITLE		Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Gilfillan,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Maki,T.W. and Rajewsky,K. Somatic hypermutation occurs in B cells of terminal deoxynucleotidyl transferase-, CD23-, interleukin-4-, Igd- and CD30-deficient mouse mutants				
JOURNAL		Eur. J. Immunol. 26 (8), 1966-1969 (1996)				
MEDLINE		96350523				
COMMENT		Automatically created by DNAPLOT version: 1.8 (1)				
FEATURES		location/Qualifiers				
source		1..355				
		/organism="Mus musculus"				
		/strain="129/SV"				
		/note="partial V-D-J region"				
		/db_xref="taxon:10090"				
		/rearranged				
		/cell_type="IgM/IgD positive B cells"				
BASE COUNT		94 a 92 c 92 g 77 t				
ORIGIN						
Query Match		60.5%; Score 279; DB 29; Length 355;				
Best Local Similarity		89.3%; Pred. No. 1.09e-188;				
Matches 317; Conservative		0; Mismatches 38; Indels 0; Gaps 0;				
Db	1	CAGGTCACACCTGACACCTGGGGCTGAGCTGGGAGACCTGGGGCTCTAGTGAAGT	60			
Qy	58	CAGGCTTATCTACACACCTCTGGGGCTAGCGTGGAGAGTCTGAGTGAAGT	117			
Db	61	TCTTCAGAGGCTTCGGGTACACATTATTCACAGTTATGACATGCGGTAAAGACACA	120			
Qy	118	TCTTCAGAGGCTTCGGGTACACATTATTCACAGTTATGACATGCGGTAAAGACACA	177			
Db	121	CCTGCACAGGGCTTGAATGATGGAGCTATTTATCCAGAAATGTGATATCTCTAC	180			
Qy	178	CCTGCACAGGGCTTGAATGATGGAGCTATTTATCCAGAAATGTGATATCTCTAC	237			
Db	181	AATCAGAGTTTAAAGGCAAGGCAATGATGACAGCAATCCTCAGACAGCCCTAC	240			
Qy	238	AATCAGAGTTTAAAGGCAAGGCTTATGATGACAGCAATCCTCAGACAGCCCTAC	297			

Db	241	ATGACGCTCAGACAGCCTTACATCTTGAGACATCTGCAGCTCTATTACTGTGCAAGAGGGTAC	300
QY	298	ATTCGATGCACACAGCCTTGACATCTGAACAGCTCTGGGGCTATTCTGTGCAAGAGGGAAC	357
Db	301	TAGCGTACTACTCTTGTGACTGTGGGGCCAGACACCACTCATCGAGCTCCGTAC	355
QY	358	TGGAGGGTGTCTGTGACTACTGTGGGGTTAAGAGAACCTTAGTCACCGCTCTCTCAG	412

RESULT	10.
LOCUS	MMMD1C 358 bp RNA ROD 20-DEC-1996
DEFINITION	M.musculus mRNA for rearranged Ig heavy chain V region (J588 family; 129MD.01c).
ACCESSION	FJ3357
NID	g1322156
KEYWORDS	antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryote; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 358)
AUTHORS	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffillan,S., Fujiswara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K.
TITLE	Somatic Hypermutation occurs in B cells of Tdt, CD23, IL-4, IgD and CD30 deficient mouse mutants
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 358)
AUTHORS	Mueller,W.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAY-1996) Mueller W., Institute for Genetics at the University of Cologne, Weyertal 121, Cologne 50931, Germany
REFERENCE	3 (bases 1 to 358)
AUTHORS	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffillan,S., Fujiswara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K.
TITLE	Somatic hypermutation occurs in B cells of terminal deoxynucleotidyl transferase-, CD23-, interleukin-4-, IgD- and CD30-deficient mouse mutants
JOURNAL	Eur. J. Immunol. 26 (8), 1966-1969 (1996)
MEDLINE	96350523
COMMENT	Automatically created by DNAPLOT version: 1.8 (1) http://www.genetik.uni-koeln.de/dnaplot .
FEATURES	Location/Qualifiers
SOURCE	1..358
	/organism="Mus musculus"
	/strain="129/SV"
	/note="partial V-D-J region"
	/db_xref="taxon:10090"
	/rearranged
	/cell_type="IgM/IgD positive B cells"
BASE COUNT	93 a 96 g 79 t
ORIGIN	

Query Match	60.1%	Score 277	DB 29	Length 358
Best Local Similarity	90.8%	Pred. No. 4,10e-187		
Matches 325; Conservative	0;	Mismatches 30;	Indels 3;	Gaps 2;

Db	1	CAGGTCACATGCACACACCTGGGGCTGAGCTGGTGAAGCCTGGGGCTCGATGAAGATG	60
QY	58	CAGGCTTATCTACACACATCTGGGGCTAGCTGTGAGAGTCTGGGGCTCATGTGAAGATG	117
Db	61	TCTTCGACAGGCTTCTGGCTACACATTTACCACTTACCAATATGCACTGGTAAAGCAGACA	120
QY	118	TCTTCGACAGGCTTCTGGCTACACATTTACCAATATGCACTGGTAAAGCAGACA	177
Db	121	CCTGCACAGGGCTTCGATGATGGAGCTATTATATCAGAGAAATGGTATCTTCTAC	180
QY	178	CCTGCACAGGGCTTCGATGATGGAGCTATTATATCAGAGAAATGGTATCTTCTAC	237

Db 181 AATCAGAGTTCGAAGGCAAGGCCATCTGCTGACAGAAATCTCTCCAGACGCTTAC 240
 OY 238 AATCAGAAATTTCAGGAGGAGGCTTATGACGACAGACATCTCCAGACGCTTAC 297
 Db 241 ATGCAAGCTCAGACGCTGACATCTGAGACTCGGGCTATTACTGTCAGAGAGGCTC 300
 OY 298 ATGCAAGATAGACGCTGACATCTGAGACTCTGGCTATTCTTCTGTCAGAGAGGAC 357
 Db 301 TATGCTAATCTAGCTTGTGACTACTGAGGCTCAAGAACTCAGTCAACGCTCTCTCAG 358
 OY 358 TG-GGAGGGTGC--TCTGACTACTGAGGCTCAAGAACTCAGTCAACGCTCTCTCAG 412

RESULT 11
 LOCUS MAMD50C 352 bp RNA ROD 20-DEC-1996
 DEFINITION M.musculus mRNA for rearranged Ig heavy chain V region (3588
 accession 273339
 family: 129MD.50C).
 91322173
 N
 KEYWORDS antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 352)
 Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Gilfillan,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K. Somatic Hypermutation occurs in B cells of Tdr, CD23, IL-4, Igd and CD30 deficient mouse mutants
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 352)
 Mueller,W. Direct Submission
 JOURNAL Submitted (14-MAY-1996) Mueller W., Institute for Genetics at the University of Cologne, Weyerl 121, Cologne 50931, Germany
 3 (bases 1 to 352)
 Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Gilfillan,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K. Somatic hypermutation occurs in B cells of terminal deoxynucleotidyl transferase-, CD23-, interleukin-4-, Igd- and CD30-deficient mouse mutants
 Eur. J. Immunol. 26 (8), 1966-1969 (1996)
 96350523
 MEDLINE
 COMMENT Automatically created by DNAPLOT version: 1.8 (1)
 http://www.genetik.uni-koeln.de/dnaplot.
 FEATURES
 SOURCE Location/Qualifiers
 1..352
 /organism="Mus musculus"
 /strain="129/SV"
 /note="partial V-D-J region"
 /db_xref="taxon:10090"
 /rearranged
 /cell_type="IgM/IgD positive B cells"
 92 a 91 c 94 g 73 t 2 others

BASE COUNT
 ORIGIN
 Query Match 59.9%; Score 276; DB 29; Length 352;
 Best Local Similarity 90.7%; Pred. No. 2,51e-186;
 Matches 322; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Db 1 CAGGTGCAACGTCGACGACCCGCGGCTAGCTGTGAGAGCTGGGCGCTCAGTGAAGATG 60
 OY 58 CAGGCTATCTACAGCATCTGGGCTAGCTGTGAGAGCTGGGCGCTCAGTGAAGATG 117
 Db 61 TCTGCAAGGCTTCTGGCTACACATTTACAGTTACATATGCACTGGGTAAAGAGACA 120
 OY 118 TCTGCAAGGCTTCTGGCTACACATTTACAGTTACATATGCACTGGGTAAAGAGACA 177

Db 121 CCTGACAGAGGCTCGGAATGATGAGCTATTATTCAGAGAAATGTAATCTCTTAC 180
 OY 178 CTTGGACAGAGGCTCTGAATGATGATGAAATATTTCTCGAAATGGTATCTTACTAC 237
 Db 181 AATCAGAGTTCGAAGGCAAGGCCATCTGACTGACAGCAAAATCTCTCAGACGCTTAC 240
 OY 238 AATCAGAAATTTCAGGAGGAGGCTTATGACGACAGACATCTCCAGACGCTTAC 297
 Db 241 ATGCAAGCTCAGACGCTGACATCTGAGACGCTGCTGCTATTTACTGTGCAAGAGACAC 300
 OY 298 ATGCAAGATAGACGCTGACATCTGAGACTCTGGCTATTCTTCTGTCAGAGAGGAC 357
 Db 301 TCGG--GCCCTATGACTACTGAGGCTCAGAGAACTCAGTCAACGCTCTCTCAG 352
 OY 358 TGGAGGGTGTCTCTGACTACTGAGGCTCAGAGAACTCAGTCAACGCTCTCTCAG 412

RESULT 12
 LOCUS AF045892 416 bp mRNA ROD 19-FEB-1998
 DEFINITION Mus musculus Ig2a heavy chain mAb12-1A VH domain mRNA, partial cds.
 accession AF045892
 nid 92895948
 NID 92895948
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 416)
 Che,Z., Olson,N.H., Mosser,A.G., Leipe,D., Rueckert,R.R., Baker,T.S. and Smith,T.J. Antibody-mediated neutralization of human rhinovirus 14 explored by means of cryo-electron microscopy and X-ray crystallography of virus-Fab complexes
 JOURNAL J. Virol. (1998) In press
 REFERENCE 2 (bases 1 to 416)
 Che,Z. and Smith,T.J. Direct Submission
 JOURNAL Submitted (04-FEB-1998) Biol. Sciences, Purdue University, Lilly Hall B135, West Lafayette, IN 47907, USA

FEATURES
 SOURCE Location/Qualifiers
 1..416
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 1..416
 V.region
 CDS
 <1..>416
 /note="VH domain; binds to M1m-1A loop to neutralize human rhinovirus 14"
 /codon_start=1
 /product="Ig2a heavy chain mAb12-1A"
 /db_xref="E02895949"
 /translation="VHSGQLQSGAEIVRPSSVKRISCKASGYAFSSYWMNVKORP GQGLWVIGQIVPEDGDNKRNKRGKRAALTAADSSSTAYWQLSLTSEDSAYVFCARS GNPVYMDYWGQSTVSVSSAKTAPASVPLAPLSIG"
 100 a 105 c 116 g 95 t

BASE COUNT
 ORIGIN
 Query Match 59.7%; Score 275; DB 29; Length 416;
 Best Local Similarity 84.9%; Pred. No. 1,54e-185;
 Matches 353; Conservative 0; Mismatches 60; Indels 3; Gaps 2;

Db 1 GTCCATCCCAAGGCTGCTGACAGCACTGGGCTAGCTGTGAGAGCCGGGCTCTCA 60
 OY 49 GTCCATCCCAAGGCTTATCTACACAGCTGGGCTAGCTGTGAGAGCTGGGCTCTCA 108
 Db 61 GTGAGATTCTCTGCAAGGCTTCTGCTATGCAATCTAGTACTGATGATGATGATG 120
 OY 109 GTGAGATGCTCTGCAAGGCTTCTGCTATGCAATGATGATGATGATGATGATG 168
 Db 121 AAGCAGAGGCTTGACAGAGGCTTCTGATGATGATGATGATGATGATGATGATG 180
 OY 169 AAGCAGAGGCTTGACAGAGGCTTCTGATGATGATGATGATGATGATGATGATG 228

[illegible]

Oy	1	ATGGAAATCAGACTGGGCTTTTCTCTTCCTCCGTGCATAAATACAGATGCTCACGCCAG	60
Db	109	GTTCAAGCTTACAGACGTCTGGGGCTGAACACTGGGCGCTCAGTAAGATGTC	168
Oy	61	GCTTATCTTACAGACAGTCTGGGGCTGAGCTGGTAGAGTCTGGGGCTCAGTAAGATGTC	120
Db	169	TGCAAGGCTTGCTGGCTAACCTTTACTGCCCTACCTGAGTGCACCTGGTAAACAGAGGCT	228
Oy	121	TGCAAGGCTTGCTGGCTAACCATGTGACCAGTTACATAATGACACTGGTAAACAGACACT	180
Db	229	GGACAGGCTCTGGAATGATGTGATACATTATCTTAACCTACCTGGTTATCTGAATACAT	288
Oy	181	GGACAGGGCCCTGGAATGATGTGAAATATTTTTCTGSAATGTGGATACTTACTACAT	240
Db	289	CAGAATCTCAAGACAGACGGCCACATGTGACTGACAGCAAATCCTCCAGCAGACCTACATG	348
Oy	241	CAGAATGTTAAGGGCCAAGGCTCTATGACTGACAGACATCCTCCAGCAGACCTACATG	300
Db	349	CAACTGACACACCTGACATCTTGAGGACTCTGACGTCTTATTGTACAAGAAGCTACTAT	408
Oy	301	CAGATCAGACACCTGACATCTGGAAGACCTCGGGCTATTTCTGTGCAAGAGG-----	354
Db	409	AACATCAGAGGGGGCTATGACTACTGGGGGTGAAGAACTGATGACCGTCCCTCAGCC	468
Oy	355	AACATGAGGGGTGCTCTTGACTACTGGGGGTGAAGAACTGATGACCGTCCCTCAGCC	414
Db	469	AAAACACAGCCCCCATCGGTCTATCTCACTGCGCCCTG	505
Oy	415	AAAAAGCACCCGCCCGCTCATCTCACTGGTCCCTG	451
RESULT	14		
LOCUS	A13735	540 bp	DNA
DEFINITION	variable region of a monoclonal antibody which cross reacts with 19 known Pseudomonas aeruginosa serotypes.		
ACCESSION	A13735		
NID	g491743		
KEYWORDS	unidentified.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 540)		
AUTHORS	Domdey,H., Margel,M. and von Specht,B.U.		
TITLE	Monoclonal antibodies to Pseudomonas aeruginosa, their production and use		
JOURNAL	Patent: EP 0338395-A 3 25-OCT-1989;		
FEATURES	BEHRINGWERKE Aktiengesellschaft		
Source	Location/Qualifiers		
CDS	1..540		
	/organism="Artificial sequences"		
	64..>540		
	/product="V region monoclonal antibody,cross reacts with 19 known P.aeruginosa serotypes"		
	/db_xref="PID:g491744"		
	/translation="MERHWIFLFESTYTAGVSOVLQSGAEELAKPGASVKMSKASGYRTAYMMHWKORPQGSEWIEYIMPTNGYTEYNONPKDKATLADKSSTAYMDLSLTSEDNAVYYICRSYNNEGAMDYGCGISTVSASKITAPSVYLAPVCDDTIG"		
BASE COUNT	145 a 144 c 130 g 121 t		
ORIGIN			
Query Match	59.7%; Score 275; DB 22; Length 540;		
Best Local Similarity	83.4%; Pred. No. 1,54e-185;		
Matches	381; Conservative 0; Mismatches 70; Indels 6; Gaps 1;		
Db	64 ATGGAAGACACGTGATCTTCTCTTCCTGTTTTCAGTACTGACAGGTGCACCTCCAG	123	
Oy	1 ATGGAATCAGACTGGGCTTTTCTCTTCCTCCGTGCATAAATACAGATGCTCACGCCAG	60	
Db	124 GTTCAAGCTTACAGACATCTGGGGCTGAACACTGGGGCTCAGTAAGATGTC	183	
Oy	61 GCTTATCTTACAGACAGTCTGGGGCTGAGCTGGTAGAGTCTGGGGCTCAGTAAGATGTC	120	

 (TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MParch_n n.a. - n.a. database search, using Smith-Waterman algorithm
 P on: Sat Apr 17 15:48:10 1999; MasPar time 71.03 Seconds
 883.040 Million cell updates/sec
 Par output not generated.

Title: >US-08-836-455-3
 Description: (1-461) from US08836455.seq
 Perfect Score: 461
 N.A. Sequence: 1 ATGGGATGCGCTGCTTT.....CTGGTCCCTGGAGCTTGGG 461
 Comp: TACCTTACGTCGACCCAGAA.....GACCAGGAGCCTTCGAAACC

Scoring table: TABLE default
 Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 188442 segs, 68026449 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

n-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40

Stats: Mean 8.375; Variance 5.103; scale 1.641

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	461	100.0	461	34	T85150	Murine monoclonal ant	1.66e-296
2	314	68.1	458	1	N91146	2H7 Vh sequence.	7.28e-194
3	314	68.1	491	39	V18557	Mouse 2H7 antibody he	7.28e-194
4	314	68.1	491	40	V03926	Mouse 2H7 antibody he	7.28e-194
5	314	68.1	491	40	V18593	Mouse 2H7 antibody he	7.28e-194
6	314	68.1	491	31	T70868	2H7 heavy chain varia	7.28e-194
7	314	68.1	518	32	T56316	2H7 antibody heavy ch	7.28e-194
8	314	68.1	520	30	T51042	Coding sequence for h	7.28e-194
9	306	66.4	453	2	N70971	2H7 Vh sequence which	2.64e-188
10	279	60.5	1570	2	Q12637	Monoclonal antibody O	1.42e-167
11	275	59.7	540	1	N91645	Heavy chain of monoc	8.39e-167
12	274	59.4	1392	30	T62935	3F4 (chimeric) human	4.13e-166
13	274	59.4	1395	30	T62935	Murine anti-porcine V	4.13e-166

14	274	59.4	3400	30	T62937	3F4 human G2/G4 chime	4.13e-166
15	274	59.4	5300	30	T62938	3F4 human IgG4 expres	4.13e-166
16	273	59.2	388	7	Q43385	H-chain V-region of m	2.04e-165
17	266	57.7	408	11	Q66846	Sequence encoding the	1.43e-160
18	265	57.5	1581	8	Q48037	Monoclonal antibody M	7.01e-160
19	263	57.0	420	11	Q65631	Murine variable regio	1.70e-158
20	263	57.0	690	33	T85090	Mouse monoclonal anti	1.70e-158
21	263	57.0	9208	11	Q65629	Vector contg. TCAE 8	1.70e-158
22	261	56.6	411	24	T35051	Mab VLI7E6 heavy chai	4.10e-157
23	259	56.2	10844	7	Q43848	Plasmid pAH4808.	9.90e-156
24	258	56.0	450	1	Q04695	Heavy chain variable	4.86e-155
25	257	55.7	10704	7	Q43846	Plasmid pAH4625.	2.39e-154
26	257	55.7	11529	7	Q43844	Plasmid pAH4602.	2.39e-154
27	255	55.3	417	7	Q43843	Chimeric 128.1 Vh, mo	5.76e-153
28	255	55.3	458	3	Q15164	Vh186 region of anti-I	5.76e-153
29	253	54.9	499	29	T38509	Heavy chain coding se	1.39e-151
30	253	54.9	1553	14	Q79930	Anti-tobacco mosaic v	6.81e-151
31	252	54.7	443	1	N91820	DNA sequence of the V	6.81e-151
32	252	54.7	12132	7	Q43847	Plasmid pAH4807.	8.03e-149
33	249	54.0	453	7	Q43593	Sequence encoding mur	8.03e-149
34	248	53.8	416	34	T85854	Anti-HMFG Mab CTMO1 h	3.94e-148
35	248	53.8	420	1	N90671	DNA sequence encoding	3.94e-148
36	248	53.8	474	3	Q20380	Sequence of Vhinge ge	3.94e-148
37	247	53.6	417	39	V01097	Heavy chain variable	1.93e-147
38	247	53.6	417	3	Q30758	p64-12.	1.93e-147
39	247	53.6	1773	38	T88869	H chain subunit of Fa	9.46e-147
40	246	53.4	416	6	Q38877	CTMO1 Vh cDNA.	2.27e-145
41	244	52.9	399	16	Q90425	DNA encoding anti-idi	2.27e-145
42	244	52.9	402	16	Q90426	DNA encoding anti-idi	2.27e-145
43	244	52.9	468	2	Q12062	Sequence encoding mou	2.27e-145
44	244	52.9	468	2	Q12018	Sequence encoding mou	2.27e-145
45	243	52.7	450	7	Q43596	Sequence encoding mur	1.11e-144

ALIGNMENTS

RESULT 1
 ID T85150 standard; cDNA; 461 BP.
 AC T85150;
 DT 04-JAN-1998 (first entry)
 DE Murine monoclonal anti-idiotype antibody 11D10 Vh cDNA.
 KW Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
 KM human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
 OS Mus musculus.
 FH Key
 FT sig_peptide Location/Qualifiers
 FT 1..57 /*tag= a
 FT mat_peptide 58..461
 FT /*tag= b
 PN WO9722699-A2.
 PD 26-JUN-1997.
 PF 19-DEC-1996; U20757.
 PR 13-DEC-1996; US-575762.
 PR 20-DEC-1995; US-575762.
 PR 26-JAN-1996; US-591965.
 PI (KENT) UNIV KENTUCKY.
 PA Chatterjee M, Chatterjee SK, Foon KA;
 DR WPI: 97-341690/31.
 DR P-PSDB: W27120.
 PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 PS Claim 12: Page 94; 130pp; English.
 CC This cDNA sequence encodes the heavy chain variable region Vh
 CC (W85150) of monoclonal anti-idiotype antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with WC-10 anti-HMFG antibody to obtain an anti-idiotype
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMFG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides are claimed. Also claimed are

diagnostic kits and methods of using 11D10, 11D10 polypeptides
CC and/or 11D10 polynucleotides, including methods of creating HMGF-
CC associated tumours.
SQ Sequence 461 BP; 112 A; 121 C; 119 G; 109 T;

Query Match 100.0%; Score 461; DB 34; Length 461;
Best Local Similarity 100.0%; Pred No. 1,66e-266;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Dd 1 atggaatgcagctgggttttcttcctcctcccttgcaataactaacagglytcccacccag 60

OY 1 ATGGAATGCACCTGGGTTCCTTCTCCTCCTCGTCAATAACTAACAGGTCACACTGCCAG 60

Dd 61 gcttatctaccagcgctctgggagtgcagctggtagtgtgagtcctvgggcctaagtgaagtcc 120

OY 61 GCATTATCTACAGCAGTGCTGGGGCTGAGCTGGTAGTGCTGGGGCCTCAGTAAGAATGTCC 120

Dd 121 tgcagaagctcttgctcatcacattgccagttacaatatgacctgygtaaaagcagaccct 180

121 TGCAAAGGTTTGGCTCACATYTACCAGATTACAATATGCACTGGGTAAAGCAGACACT 180

Dd 181 ggacaaggccccgatgatgtaatgtgaatactatttcctgnaatgtgtactactatacat 240

OY 181 GGACAGGCCCCGGAATGATGTGAATAATTTTTCTCTGAAATGSGTGAATCTACTAACAAT 240

Dd 241 cagaagtttaaaggccaaggccctcatctgactgcagacacatcctccacagcctcataig 300

OY 241 CAGAAGTTTAAAGGCCAAGGCCCTCATTTGACTGCAGACACATCCTCCACAGCCTACATG 300

Dd 301 caagtcaggcagccctgacatctgaaagactctgcgtctattctctgtcaaagaygaactgg 360

OY 301 CAGATCAGACACCTGACACTCTGAAGACTCTGGGCTCATATTTCTGTGAAGAGGGAAGCTGG 360

Dd 361 gagsgtctctcgagactactggtggtcaaagaaacctcagtcacgcgtctcctcagccaag 420

OY 361 GAGSGETCTCGACACTACTGGGGGTCAAAGAACTCTCAGTACACGCTCTCTCTACGCCAAAAG 420

Dd 421 acacccccaccgctcatlccactggtccctygaacttggg 461

OY 421 ACACCCCACCCGCTCATCCACTGGTCCCTGGAAGCTTGGG 461

RESULT 2

ID N91146 standard; DNA; 458 BP.

AC N91146;

DT 06-JUL-1990 (first entry)

DB ZH7 Vn sequence.

TI Antibodies; passive immunisation: pH3-6a; ss.

OR Synthetic.

FH Key

FT cds Location/Qualifiers

FT 39..458

FT /*lag= a

FT misc_feature 398..408

FT /*tag= b

FT misc_feature /note="Sequence homologous to DSP-2"

FT FT 360..406

FT misc_feature /tag= c

FT FT /note="JHI region"

PN WO8900999-A.

PD 9-FEB-1989.

PF 25-JUL-1988; 02514.

PR 24-JUL-1987; US-077528.

PA (ITGE-) Int Genetic Eng Inc.

PI Robinson RR, Liu AY, Horwitz AH, Mail R, Better M;

DR WRI: 89-061144/08.

DR P-PADB: p94780.

PT Polynucleotide(s) encoding Immunoglobulin molecules -

PT used for efficient prodn. of chimeric human or non-human or

PS class switched antibodies.

PP Disclosure: 7pp: English.

CC Sequence carries 2H7 VH region of the chimeric immunoglobulin sequence.

CC The antibodies are useful in passive immunisation avoiding negative

C immune reactions. They are also useful in assaying and in vitro imaging.

SQ	Sequence	458 BP;	113 A;	120 C;	112 G;	113 T;
	Query Match	68.1%;	Score 314;	DB 1;	Length 458;	
	Best Local Similarity	94.6%;	Pred.No.7-28e-194;			
	Matches	333;	Conservative	0;	Mismatches 19;	Indels 0; Gaps 0
Dd	atggagctcagcaagatcttctcttcctcctgtcagtaactacaagtgtccacctccag	98				
Oy	1 ATGGATACCACTGGGTCCTTCTCCTCTCTCCCTGTCAATAACTACAGGTCCTCACG	60				
Dd	gcttatcacacagcagctcgcggcgctgaagctgttgaggcctggcgctcagaigaatgcc	158				
Oy	61 GCTTATTCTACACGACTCTGGGGCTGAAGTGAGTGGAGGTCGGGGCTCATGAATATGCC	120				
Dd	tgcaggctcttgctctacacattaccagttacacatatgcactggtglaaagcacacact	218				
Oy	121 TGCAAGCGTTCTGGCTACACTTGACCAGATTACAAATATGCCTGGTAAACACACACT	180				
Dd	agacagggcctggaatgatgtgtagctattatccagaanaatgltgtaacttctaacaat	278				
Oy	181 GGACAGCGGCTCGTAATGATTTGAAATATTTTCTCGTAATGATGATCTTACTTACAAT	240				
Dd	cagaagtccaaggcgcaagggccacactgactgtataacaatctccagacagcctaatg	338				
Oy	241 CAGAAGCTTAAAGGGCGAAGGCTCCTCAATTGACTGTCAACACACATCTCCACACAGCCTACATG	300				
Dd	cagctcagcagcctgtacactcgaagactctggctcatcttctgtgcaagag	390				
Oy	301 CAGATCACACACCTGTGACATCTGAAGACTCTCGGTCATTCTGTGTGCAAGAG	352				
RESULT	3					
ID	V18557 standard; cDNA; 491 BP.					
AC	V18557:					
DT	05-JUN-1998 (first entry)					
DE	Mouse 2H7 antibody heavy chain variable region cDNA.					
KW	Mouse; murine; heavy chain; variable region;					
RW	immunoglobulin fragment production; Ig fragment production;					
KM	monoclonal antibody 2H7; human B-cell surface antigen; ss.					
OS	Mus sp.					
FH	Key	Location/Qualifiers				
FT	sig_peptide	72..128				
FT	/*tag= a	129..491				
FT	mat_peptide	/+tag= b				
PN	US5698435-A.					
PD	16-DEC-1987.					
PF	06-JUN-1995; 467140.					
PR	29-MAR-1990; US-501092.					
PR	01-NOV-1985; US-793980.					
PR	27-OCT-1986; WO-002269.					
PR	24-JUL-1987; US-077528					
PR	11-JAN-1988; US-142039.					
PR	08-DEC-1992; US-987535.					
PR	18-AUG-1994; US-299085.					
PR	06-JUN-1995; US-467140.					
PA	(XOMA) XOMA CORP.					
PI	Better M. Horwitz AH, Lei S, Liu AY, Robinson RM, .					
PI	Wall R, Wilcox GL;					
DR	WPI; 98-051492/05.					
DR	P-PDSB; W47513.					
PT	DNA encoding secretable immunoglobulin fragments - comprising at					
PS	least the variable regions of light or heavy chains					
CC	Example IV; Fig 21: 98pp; English.					
CC	The present sequence was used in the development of a novel method					
CC	for the production of an immunoglobulin (Ig) fragment capable of					
CC	binding an antigen. The method comprises culturing an E. coli host					
CC	cell has been transformed with a nucleic acid molecule encoding the					
CC	Ig fragment, under conditions so that the Ig fragment is produced					
CC	and secreted. The nucleic acid molecule comprises DNA sequences					
CC	encoding: (a) pectate lyase secretion signal sequence operably					
CC	linked to a DNA sequence encoding at least the variable region of					
CC	an Ig Fd molecule; and (b) pectate lyase secretion signal sequence					

operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a novel approach for producing genetically engineered antibodies of desired variable region specificity and constant region properties. The cloned Ig gene products can be produced by expression in genetically engineered organisms. The application of chemical gene synthetesis, recombinant DNA cloning and production of specific Ig chains in various organisms provides an effective solution for the efficient large scale production of human monoclonal antibodies. The invention also provides a solution to the problem of class switching antibody molecules.

Sequence 491 BP; 113 A; 152 C; 113 G; 113 T;

Query Match	68.1%;	Score 314;	DB 39;	Length 491;
Best Local Similarity	94.6%;	Pred. No. 7.28e-194;		
Matches 333; Conservative		0; Mismatches 19;	Indels 0;	Gaps 0;

131
 132 atggatctcaagcaggaacctctctctccctctcagtaactcaacagatgccaactccag 131
 133 |||||
 QY 1 ATGGAATGCAAGCTGGGCTTCTCTCTCTCTGTCATTAATCAAGGTGCCATCTCCAG 60
 Db 132 gcttatctacagcagctctctgggctgagctggtgagggcctgggacctgaatgagatgtcc 191
 QY 61 GCTTATCTACAGCAGCTTGGGGCTGAGACTGGTAGGCTGGGGCTCCAGTGAAGATGTCC 120
 Db 192 tgcgaagctctctgctacacattaccagctacaattgacctgggtggaagcagaaacct 251
 QY 121 TGCAGGCTTCTGGCTACATTGACCAAGTTACAAATGCACTGGGTGAAGCAGACACT 180
 Db 252 agcagaggccttgaaatggaattgagctattatccagaagaaatggtgtaactgctcaat 311
 QY 181 GGAGAGGGCCCTGGATATGATTTGGAATATTTTCTCGGAATGGTGATTTACTTCTCAAT 240
 Db 312 cagaagctcaagggcgaagccacacatgctacgtatgagacaatccctccacacagactaatg 371
 QY 241 CAGAAGTTTAAGGGCAGGCGCTATTGACTGCAGACACATCTTCAGACACAGCTTCAATG 300
 Db 372 cagctcagcagcctgacatctgaagactctggtgctattctgtgcaagag 423
 QY 301 CAGATTCAGACGCTGACATCTGAAGATCTCGCGCTATTCTGTGGAAG 352

RESULT 4
V03926 standard; cDNA; 491 BP.

ID	Accession	Location/Qualifiers
DE	01-JUN-1998	(first entry)
DE	Mouse 2H7	mouse variable region cDNA.
KM	Mouse; murine; heavy chain; variable region;	
KW	Immunoglobulin fragment production; Ig fragment production;	
KW	monoclonal antibody 2H7; human B-cell surface antigen; ss.	
OS	Mus sp.	
EH	Key	
FT	sig_peptide	72..128
FT		/*tag= a
FT	mat_peptide	129..491
FT		/*tag= b
PN	US5693493-A.	
PD	02-DEC-1997.	
PE	25-MAY-1995.	450731.
PR	29-MAR-1980.	US-501092.
PR	01-NOV-1985.	US-793980.
PR	27-OCT-1986.	WO-002269.
PR	24-JUL-1987.	US-077528.
PR	11-JAN-1988.	US-142039.
PR	08-DEC-1992.	US-987555.
PR	18-AUG-1994.	US-299085.
PR	25-MAY-1995.	US-450731.
PA	(XOMA) XOMA CORP.	
PA	Belter M, Horwitz AH, Lei S, Liu AY, Robinson RR.	

PI Wall R, Wilcox GL;
DR WPI; 98-031749/03.
P-PSDB; W41070.
PT Production of chimeric antibody fragments - by culturing E. coli
transformed with dicistronic expression cassette

CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.

Sequence 491 BP; 113 A; 152 C; 113 G; 113 T;

Query Match	68.1%	Score 314;	DB 40;	Length 491;
Best Local Similarity	94.6%	Pred. No. 7.28e-194;		
Matches 333;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;

Db	72	atggagctcagcagagatcttctctctccctcctcgtcagtaactaagttgtccactccag	133
Qy	1	ATGGATCACCACCTGGGCTTCTCTCTCTCTCTCTGTCATAATCACAGGTGCCACTCCAG	60
Db	132	gctatctcacagcagctctggggcctgagctgtgagggccttggggcctaaagtggaagtcc	191
Qy	61	GCTATCTACACGACGCTGGGGGCTGCAGCTGGTGAGGCTGGGGGCTTAGTGAAGATGTC	120
Db	192	tgcgaagctcttggtctacacattaccagttacacaatagcactggtgtaagcagacact	251
Qy	121	TGCAGGCTTTGGCTACACATTACCAAGTTACATATTGCACGTGGTAAACGACACACT	180
Db	252	agacagggccctggaatggaattggaagctattatccacgaagaatgtgtacttgcataat	311
Qy	181	GGACAGGGCCGTGGAAATGATTTGGAAATATTTTCTGGAAATGCTACTTACTTACAAT	240
Db	312	cagaagttcaaggcgaagccacacactgactgttagacaatctccacgacagcctacatg	371
Qy	241	CAGAAGTTTAAGGGCAGAGGCTCATTTGACTGCACAGACATCTCCACACAGCCTACATG	300
Db	372	cagctcagcagccctgacatctggaagatctcgggtctcatcttctgtgtaagag	431
Qy	301	CAGATCCACACCTTGACATCTGGAAGACTCTGGCTTATTTCTGTGCAAGG	360

RESULT	5
ID	V18593 standard; CDNA; 491 BP.

DE		
DT	05-JUN-1998	(first entry)
DD	Mouse 2H7 antibody heavy chain variable region CDNA.	
KW	Mouse; murine; heavy chain; variable region;	
KW	immunoglobulin fragment production; ig fragment production;	
KW	monoclonal antibody 2H7; human B-cell surface antigen; ss.	
OS	Mus sp.	
FT	Key	Location/Qualifiers
FT	sig-peptide	72..128
FT		/*tag= a


```

QY 181 GCACAGGCGCTGGAATGATTTGGAATATTTTCCTGGAAATGCGATCTACTACTACAT 240
Db 312 cagaagttcaaggcgaagccacactgactgtagaacaatccctccagcagcctacatg 371
QY 241 CAGAAGTTTAAGGCGCAAGGCGCTCATTTGACTGCAGACACATCTCTCCAGACAGCCTACATG 300
Db 372 cagctcagcagcctgcagactctgaagactctcggtctattctctgtgcaagag 423
QY 301 CAGATCAGACCGCTGCACATCTGAAGACTCTCGGCTATTTCTGTGCAAGAG 352

RESULT
ID T36316 standard; cDNA; 518 BP.
AC T36316;
DE 21-OCT-1997 (first entry)
KW 2H7 antibody heavy chain variable region cDNA.
KW Immunoglobulin G; IgG; heavy chain; recombinant production;
KW antibody; passive immunisation; serum sickness; anaphylactic shock;
KW immunosassay; imaging; reagent; complement mediated lysis;
KW therapy; variable region; ss.
Mus spp.
Key Location/Qualifiers
FT signal_peptide 71..127
FT mat_peptide /*tag= a
FT /*tag= b
FT 128..490
PN US5595898-A.
PD 21-JAN-1997.
PE 01-NOV-1985; 793980.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PA (XOMA ) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
DR WPI: 97-107579/10.
DR P-PSDB; W10588.
PT Nucleic acid encoding immunoglobulin fragment - comprising
PT di:clstronic transcription unit with pectate lyase signal sequences
PS Example; Fig 21, 95pp; English.
CC The present sequence encodes the heavy chain variable region of
CC the 2H7 antibody. The 2H7 cDNA was used in the preparation of
CC a novel polynucleotide molecule encoding an Ig fragment. The DNA
CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC secretion signal sequences respectively linked to a DNA sequence
CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC single prokaryotic promoter so as to form a dicistronic
CC transcription unit, provided that the Ig fragment can bind an
CC antigen and is produced and secreted by an E. coli host cell when
CC the nucleic acid molecule is expressed in the host cell.
CC The polynucleotide molecule is used for the production of
CC recombinant antibodies, which can be used for passive immunisation
CC without negative immune reactions (e.g. serum sickness and
CC anaphylactic shock), in labelled forms as immunosassay or imaging
CC reagents, in complement mediated lysis and for therapeutic
CC purposes when coupled to a toxin or other therapeutic agent.
SQ Sequence 518 BP; 113 A; 152 C; 140 G; 113 T;

Query Match 68.1%; Score 314; DB 32; Length 518;
Best Local Similarity 94.6%; Pred. No. 7.28e-194;
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```

```

Db 191 tcaagcttcctgctcacacattaccaggttaacatgacgtggttaagcagacact 250
QY 121 TGCAAGCTTCTGGCTACACATTCAGATTCATATGCACTGGGTAAAGACAGACACT 180
Db 251 agacagggcctggaatgatgagctattatccagaagatgtagtactctacaat 310
QY 181 GCACAGGCGCTGGAATGATTTGGAATATTTTCCTGGAAATGCGATCTACTACTACAT 240
Db 311 cagaagttcaaggcgaagccacactgactgtagaacaatccctccagcagcctacatg 370
QY 241 CAGAAGTTTAAGGCGCAAGGCGCTCATTTGACTGCAGACACATCTCTCCAGACAGCCTACATG 300
Db 371 cagctcagcagcctgcagactctgaagactctcggtctattctgtgcaagag 422
QY 301 CAGATCAGACCGCTGCACATCTGAAGACTCTCGGCTATTTCTGTGCAAGAG 352

RESULT
ID T51042 standard; cDNA; 520 BP.
AC T51042;
DE 06-AUG-1997 (first entry)
DE Coding sequence for heavy chain variable region of 2H7.
KW Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
KW protein production; human; constant region; passive immunisation; toxin;
KW serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
KW antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;
KW myeloma cell; B-cell antigen; ss.
Mus musculus.
Key Location/Qualifiers
FT cds 71..490
FT /*tag= a
FT /*product= heavy chain variable region of 2H7
FT /*note= "no stop codon given"
PN US5576195-A.
PD 19-NOV-1996.
PE 01-NOV-1985; 793980.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 29-MAR-1990; US-501092.
PR 08-DEC-1992; US-987555.
PR 22-FEB-1993; US-020671.
PR 09-DEC-1994; US-357234.
PA (XOMA ) XOMA CORP.
PI Better M. Lei S, Robinson RR, Wilcox GL;
DR WPI: 97-011254/01.
DR P-PSDB; W12042.
PT Improved prodn. of protein in Gram -ve bacteria using signal
PT sequence - from pectate lyase to ensure transport of protein from
PT the cytoplasm, esp. for prodn. of antibodies
PS Example 4; Fig 21, 86pp; English.
CC This sequence represents the coding sequence for the heavy chain variable
CC region of the 2H7 mouse monoclonal antibody. The 2H7 antibody recognises
CC the human B-cell surface antigen Bp35, which plays a role in B-cell
CC activation. This sequence was used in a human-mouse chimeric antibody
CC with human B-cell antigen specificity, that was produced using the method
CC of the invention. The method of the invention is for the production of a
CC protein in a Gram-negative bacterium. The method improves on current
CC techniques, by using a vector including DNA encoding the pectate lyase
CC signal sequence (see J51034), attached to the sequence encoding the
CC immunoglobulin (Ig), particularly those with a human constant region,
CC suitable for passive immunisation (without risk of serum sickness or
CC anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may
CC also be used therapeutically, optionally coupled to toxins, etc.
CC Alternatively the protein to be produced is the sweetener thaumatin. The
CC presence of this signal sequence means that the protein is exported from
CC the cytoplasm and can be recovered from the culture medium or periplasm,
CC in active and correctly folded form. The method allows the class of any
CC antibody to be switched, e.g. most human-human Ig are of M class, easily
CC reduced and aggregated, and these can now be changed to G, A or E

```

DR	PI	Robinson RR, Liu AY, Horwitz AH, Wall R, WPI: 87-136004/19.
DR	P-PSDB: P70627.	
PT	Prodn. of immunoglobulin chains and molecules - is by recombinant DNA procedures, with chimeric antibodies etc. related to cancer specific antigens.	
PT	Example: Fig 21: 126pp. English.	
PS	The patentors claim a chimeric antibody molecule comprising 2 light chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonucleotides (JIGS) for use as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs or genes. Depending on the nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific J sequence. UIG denotes universal immunoglobulin gene.	
CC	Sequence 459 BP; 113 A; 120 C; 112 G; 114 T;	
SQ		
Query Match	66.4%; Score 306; DB 2; Length 459;	
Best Local Similarity	94.1%; Pred. No. 2,64e-188;	
Matches	332; Conservative 0; Mismatches 20; Indels 1; Gaps 1	
Db	39 atggagatcagcagagatcttctcttcctcctcgtcagtaactaagaagtgcactccca	98
QY	1 ATGAGATGCACACTGGGCTTTCTCTCTCTCTGTCATTAATACACAG-GGTGCACCTCCA	59
Db	99 ggctattatcaagaagcttggagcttgagctgtgtaagccttgagccctcagtgaaatgtc	158
QY	60 GCGTTATATACAGCAGTGTGGGCTGAGCTGTGAAGTCTGGGCTTCAGGAAGAGTGC	119
Db	159 ctgcgaagctcttgctcacatcttaccaggttacacatgatgcactgggtlaagcagacac	218
QY	120 CTGCAAGGCTCTGGGCTACATGTGACCAAGTTAAATATGACATCGGCTAAAGCAGACAC	179
Db	219 tagacagggcctggaatggattgagctattatccaggaatggtgattcttcacaa	278
QY	180 TGGACAGGCGCTGGAATGATTTGAAATATTTTCTCGAATGATGATCTACTACAA	239
Db	279 tcgaagatcgaaggcgaagccacacagcagctgtagacaatcccccagcacagctcat	338
QY	240 TCAGAGATTTAAGGCGCAGGCTCATTTGACGACAGACACATCCCTCCAGCAGCCTTACAT	299
Db	339 gcaagctcagcagcctgcagatctgaagaactcgtggtctattctgtgcaagag	391
QY	300 GCAAGTCAAGCAGCCTGGAATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAG	352
RESULT	10	
ID	Q12637 standard; DNA; 1570 BP.	
AC	Q12637:	
DE	03-OCT-1991 (first entry)	
DR	Monoclonal antibody OK3T heavy chain coding sequence.	
KW	OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.	
OS	Mus musculus.	
FH	Key	Location/Qualifiers
FT	signal_peptide	41..97
FT		/*tag= a
FT	mat_peptide	98..1447
FT		/*tag= b
FT		/product= OK3T heavy chain
PN	MO9109967-A.	
PN	MO9109968-A.	
PD	11-JUN-1991.	
PR	21-DEC-1990; G02017.	
PR	21-DEC-1989; GB-028874.	
PR	21-DEC-1990; WO-G02017.	
PA	(CELL-) CELTECH LTD.	
PI	Adair JR, Athwal DS, Emtage JS;	
DR	WPI: 91-222915/30.	
DR	P-PSDB: R13061.	
PT	New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis	

PS Disclosure; Fig 2a; 91pp; English.
 CC The OK37 heavy chain sequence was isolated from a cDNA library
 CC prepared from OK37 producing cells. The library was screened with a
 CC probe complementary to a sequence in the mouse IgG2a constant CH1
 CC domain region. The OK37 sequence was used in CDR-grafting experiments
 CC to prepare humanised antibodies.
 SQ Sequence 1570 BP; 447 A; 443 C; 356 G; 324 T;

Query Match 60.5%; Score 279; DB 2; Length 1570;
 Best Local Similarity 82.4%; Pred. No. 1,42e-169;
 Matches 374; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Db 41 atggaagagcagcggatcttctactcctgttgcagtaagcagtgccaccocag 100
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1 ATGGAATGCAAGCTGGGCTTTCTTCTCTCTGTCATTAAGTGTCCATCCAG 60
 Db 101 gtccagctgcagcagcagctggtggtgagcagcagcagcagcagcagcagcagc 160
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGTAGCTCTGGGGCTCAGTGAAGATGTC 120
 Db 161 tgcagagctctgtgtacacaccttaagtagacagatgcaactggtgtaaacagagcct 220
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 TCGAAGCTTCTGCTACACATTGACAGATTACAAATGCTGCTGGAAGACACACT 180
 Db 221 ggcagaggtctggaatggtatgataatcctagccgttggtataataataat 280
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 181 GGCAGAGGCTCGAATGATGGAATATTTCTGGAATGCTGACTTACTACTCAAT 240
 Db 281 caaagattcaagagcaagcagcagcagcagcagcagcagcagcagcagcagcagc 340
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 241 CAAAGATTAAAGGCAAGGCTCATTCATGCGAGACACATCTCCAGCAGCCTCATG 300
 Db 341 caactagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 400
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGTATTTCTGTAAGAGGAACTGG 360
 Db 401 gacattacgccttactactctgggccaagagcaccactctcaagctctcaagcaaa 460
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 361 GAGGGTG-CT-CTGGACTACTGGGGCAAGAACTCAGTCACTCTCTCAGCCAAA 417
 Db 461 acacagcccccacatcggtctatccactgccccctg 494
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 418 ACGACACCCGCCCGCTATCCACTGCTGCTCG 451

RESULT 11
 ID N91645 standard; DNA; 540 BP.
 AC N91645;

15-MAR-1990 (first entry)
 Heavy chain of monoclonal antibody 6A4.
 KM Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.

PI Location/Qualifiers
 FT cds 64..540
 FT /tag- a

PN EP-338395-A.
 PD 25-OCT-1989.
 PF 12-APR-1989; 106463.
 PR 19-APR-1988; DE-813023.
 PA (BEHM) Behringwerke.
 PI Domdey H, Margel M, von Specht BU;
 DR WPI: 89-310861/43.
 DR P-PSDB; P93079.
 PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
 PT variable antibody regions.
 PS Claim 1; page 6; 7pp; german.
 CC The sequence has a variable and constant region. Monoclonal antibody 6A4
 CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.
 CC It is used for therapy and diagnosis of infection, and as a carrier for
 CC drugs. The antibody is IgG2a subclass.
 SQ Sequence 540 BP; 145 A; 144 C; 130 G; 121 T;

Query Match 59.7%; Score 275; DB 1; Length 540;
 Best Local Similarity 83.4%; Pred. No. 8.39e-167;

Matches 381; Conservative 0; Mismatches 70; Indels 6; Gaps 1;

Db 64 atggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 123
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 1 ATGGAATGCAAGCTGGGCTTTCTTCTCTCTGTCATTAAGTGTCCATCCAG 60
 Db 124 gtccagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 183
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGTAGGCTGTGGGGCTCAGTGAAGATGTC 120
 Db 184 tgcagagctctgtgtacacaccttaagtagacagatgcaactggtgtaaacagagcct 243
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 TCGAAGCTTCTGCTACACATTGACCAATTACAAATGCTGCTGTAAGACAGACACT 180
 Db 244 ggcagaggtctggaatggtatgataatccttaacacagcagcagcagcagcagcagc 303
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 181 GGCAGAGGCTCGAATGATGGAATATTTCTGGAATGCTGATTAATCTACTCAAA 240
 Db 304 cgaagattcaagagcaagcagcagcagcagcagcagcagcagcagcagcagcagc 363
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 241 CAAAGATTAAAGGCAAGGCTCATTCATGACGACACATCTCCAGCAGCCTCATG 300
 Db 364 caactagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 423
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGTATTTCTGTCAGAGAGG----- 354
 Db 424 aactagagagggctatgactactggtggtcaagagcagcagcagcagcagcagcagc 483
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 355 AACTGGAGAGGCTCTGTGACTACTGGGGCAAGAACTCAGTCACTCTCTCAGGC 414
 Db 484 aaacacagcagccacatcggtctatccactgccccctg 520
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 415 AAACGACACCCGCCCGCTATCCACTGCTGCTCG 451

RESULT 12
 ID T62936 standard; CDNA; 1392 BP.

AC T62936;
 DT 16-JUN-1997 (first entry)

DE 3F4 (Chimeric) human G2/G4 chimeric antibody cDNA.
 KM Xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis; ss.
 OS Chimeric Homo sapiens;

OS Chimeric Mus sp.
 PN MO9711971-A1.

PD 03-APR-1997.
 PF 27-SEP-1996; U15575.

PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.

PA (ALEX-) ALEXION PHARM INC.
 PI Evans WJ, Matis LA, Mueller EE, Mueller JP, Rollins S;

PI Rother RP;
 DR WPI: 97-212855/19.

DR P-PSDB; W14939.
 PT Antibodies binding to porcine but not human cell interaction

PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 56-57; 105pp; English.

CC A cDNA clone (T62936) codes for a chimeric antibody (W14939)
 CC comprising the C1 and hinge regions of human IgG2 and the C2 and C3

CC regions of human IgG4 (G2/G4 Mab) and a murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb)

CC 3F4 heavy chain variable region sequence (see also T62938). A 3F4
 CC human G2/G4 expression plasmid insert sequence is provided in

CC T62937. The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants

CC and for improving xenotransplantation of porcine cells, tissues and
 CC organs into human recipients.

SQ Sequence 1392 BP; 320 A; 433 C; 377 G; 262 T;

Query Match 59.4%; Score 274; DB 30; Length 1392;
 Best Local Similarity 81.8%; Pred. No. 4.13e-166;

OY 241 CAGAGTTTAAAGGCAAGGCGCTATTGACTGCAGACACATCCTCCAGCAGACTACATG 300
Db 1650 caactcaagcagcttggcatctgaggaactctggtctctattactgtgcaagacgtacgta 1709
OY 301 CAGATCAGCAGCGCTGACATCTGAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAC-TG 359
Db 1710 ggaagctacttg-actactggggccaagggcaccaactctcacagctctcctcagcctcac 1768
OY 360 GGAGGGTGTCTGTGACTACTGGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCAGCCAANAAC 419
Db 1769 caaaggccccatccgctctcccccctgg 1794
OY 420 GACACCCCGCCCGCTGTATCCACTGG 445

Search completed: Sat Apr 17 15:51:42 1999
Job time : 212 secs.

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 15 18:00:56 1999; MasPar time 8.71 Seconds
 Parallel output not generated. 657.976 Million cell updates/second

```
Title: >US-08-836-455-4
Description: (1-153) from US08836455.pep
Perfect Score: 1109
Sequence: I MECSWVFLFLSLITTVGHNS.....TVSSAKTTPPPVYPLVPGSL 153
```

Scoring table: PAM 150

Searched: 116695 seqs, 37453910 residues

```
Post-processing: Minimum Match 08
Listing first 45 summaries
```

Database: pir58

Statistics: Mean 42.120; Variance 104.479; scale 0.403

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

id	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	783	70.6	475	2	S01321	Ig gamma-2b chain pre	4.38e-10
2	780	70.3	474	2	S25057	Ig gamma-2b chain - m	1.38e-10
3	774	69.8	469	2	S37483	Ig gamma-2a chain - m	1.37e-10
4	767	69.2	151	2	PL0011	Ig heavy chain precut	2.00e-10
5	763	68.8	150	2	PN0444	Ig heavy chain V regi	9.21e-10
6	746	67.3	139	2	PS0024	Ig heavy chain precut	6.10e-10
7	742	66.9	166	2	PL0012	Ig heavy chain precut	2.81e-99
8	727	65.6	137	2	H33513	Ig heavy chain precut	8.57e-97
9	724	65.3	232	2	S38950	Ig gamma chain - mous	2.69e-96
10	724	65.3	446	2	S42095	Ig gamma-2a chain (ma	5.57e-94
11	710	64.0	178	2	S29594	Ig gamma chain (NM65)	8.15e-94
12	709	63.9	140	1	HNWSG7	Ig heavy chain precut	1.19e-93
13	708	63.8	138	2	S21810	Ig heavy chain V regi	3.74e-93
14	705	63.6	140	2	PH1489	Ig heavy chain V regi	7.84e-92
15	697	62.8	140	2	PH1482	Ig heavy chain V regi	5.25e-91
16	682	62.4	138	2	E33513	Ig heavy chain precut	5.13e-90
17	685	61.9	140	2	PH1488	Ig heavy chain V regi	7.50e-90
18	685	61.8	136	2	PL0208	Ig heavy chain precut	1.10e-89
19	684	61.7	141	2	A33276	Ig heavy chain precut	3.43e-88
20	681	61.4	140	2	PH1484	Ig heavy chain V regi	1.07e-88
21	678	61.1	139	2	A27609	Ig heavy chain precut	2.29e-88
22	676	61.0	135	2	A30577	Ig heavy chain precut	3.34e-88
23	675	60.9	135	2	PS0057	Ig heavy chain precut	

24	675	60.9	140	2	PH1488	Ig heavy chain V reg1	3.34e-88
25	672	60.6	135	2	PH1493	Ig heavy chain V reg1	1.04e-87
26	671	60.5	137	2	PH1227	Ig heavy chain precut	1.53e-87
27	670	60.4	135	2	PH1454	Ig heavy chain V reg1	2.23e-87
28	670	60.4	135	2	PH1452	Ig heavy chain V reg1	2.23e-87
29	668	60.2	140	2	PH1486	Ig heavy chain V reg1	4.76e-87
30	664	59.9	140	2	PH1483	Ig heavy chain V reg1	2.17e-88
31	661	59.6	117	2	SC03289	Ig heavy chain precut	6.77e-88
32	661	59.6	133	2	PC1155	Ig heavy chain precut	6.77e-88
33	658	59.6	140	2	A6194	Ig heavy chain V reg1	2.11e-88
34	655	59.1	139	1	MMHS1	Ig heavy chain precut	6.58e-88
35	653	58.9	141	2	J10076	Ig heavy chain precut	1.40e-88
36	651	58.7	137	2	E29380	Ig heavy chain precut	2.99e-88
37	650	58.6	137	2	E29380	Ig heavy chain precut	4.37e-88
38	645	58.2	117	1	HYMSA1	Ig heavy chain precut	2.90e-88
39	645	58.2	136	2	SO4576	Ig heavy chain precut	2.90e-88
40	642	57.9	131	2	A27476	Ig heavy chain precut	9.03e-88
41	642	57.9	140	2	SO4575	Ig heavy chain precut	9.03e-88
42	637	57.4	136	2	B47159	Ig heavy chain V reg1	5.98e-88
43	636	57.3	117	1	GMMS4	Ig heavy chain precut	8.73e-88
44	635	57.3	137	1	GMMS3	Ig heavy chain precut	1.27e-88
45	634	57.2	117	1	HWS3	Ig heavy chain precut	1.86e-88

ALIGNMENTS

ENTRY	1	S01321	#type complete
TITLE		Ig gamma-2b chain precursor - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		30-Sep-1989 #sequence_revision 30-Sep-1989	#text_change
ACCESSIONS		S01321	
REFERENCE		S01320	
#authors		de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.	
#journal		Eur. J. Biochem. (1988) 176:287-295	
#title		Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.	
#cross-references		MUID:88329081	
#accession		S01321	
#molecule_type		mRNA	
#residues		1-475	#label DEL
#cross-references		EMBL:X13188; NID:g51780; PID:g51781	
#note		this sequence was determined from the differentiated gene	
CLASSIFICATION		#superfamily immunoglobulin C region; immunoglobulin homology	
KEYWORDS		immunoglobulin	
FEATURES			
1-19			
20-475		#domain signal sequence #status predicted #label SIG	
159-223		#product Ig gamma-2b chain #status predicted #label MATV	
		#domain immunoglobulin homology #label IGG1	
SUMMARY		#length 475 #molecular-weight 51567 #checksum 4120	
Query Match		70.6%;	Score 783; DB 2; Length 475;
Best Local Similarity		71.4%;	Pied. No. 4,38e+106;
Matches		110; Conservative	22; Mismatches 18; Indels 4; Gaps 3;
Dd	1	MEMWIFLFLSTAGQSOVOLQOOGAELARPASVKLSCKASGYTLTSIGISWKORT	60
Oy	1	MECSWYFLFLSLTTGVHQAIVYIQSGALDVNSGASVKMKSCASATYTLTYSIMHHVKRTP	60
Dd	61	GQGLEWTIGEITPSSGSNYENEKFKGATLTVDKSSSTAYLAHLSSITSDEDAVFCA-GPR	119
Oy	61	GQGLEWTIGNFEPPNGDTIYNQKFGKASLTADTSSSTAYMAQISSITSDESAVFFCARGNW	120
Dd	120	OVGLLPFGYGQGTLTVAASAARTPSVPLAPG	153
Oy	121	E-GAL--DYWGQGSTVTVASAKTTPPVYPLVPG	151
RESULT	2		

```
ENTRY          S25057      #type complete
TITLE          Ig gamma-2b chain - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
              31-Oct-1997
ACCESSIONS     S25057
REFERENCE       S25057
AUTHORS        Fischer, R.; Voss, A.; Niersbach, M.; Muzliker, W.; Hirsch,
              H.U.; Kreuzaler, F.
#submission    submitted to the EMBL Data Library, July 1992
#description    Production of a Tobacco mosaic virus (TMV) inactivating
              neotop specific monoclonal antibody in Nicotiana tabacum.
#accession     S25057
#status        preliminary
#molecule_type mRNA
#residues      1-474 ##label FIS
#cross-references EMBL:X67210; NID:954826; PID:954827
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
              #length 474 #molecular-weight 52069 #checksum 4891
SUMMARY
Query Match          70.3%; Score 780; DB 2; Length 474;
Best Local Similarity 71.1%; Pred. No. 1.38e-105;
Matches 108; Conservative 21; Mismatches 21; Indels 2; Gaps 2;

DB 1 MEMSWFLFLSGTAGHSEVQLOOSGPELVNPGASVSKSCASGYTFTYVHWKQKP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1 MECSWFLFLSLTTTGVSQAYLOOSGAEIVRSASVSKSCASGYTFTYVHWKQKP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GGGLEWIGYINPNKDGTFENKFKATLTSDKSNATVAMELSLTSEDSAYVCARDY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 GGGLEWIGNIFPENGDTYVNOFKKASLTADTSSSTAYVMOISLTSEDSAYVFCARG-N 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 YD-WFAYWQGTILVYSAKTTPPSYPLAPG 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 WEGALDYWGQGTSVTVSSAKTTPPYVPLVPG 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT          3
ENTRY          S37483      #type complete
TITLE          Ig gamma-2a chain - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              08-Sep-1997
ACCESSIONS     S37483
REFERENCE       S37483
AUTHORS        Ducancel, F.F.D.
#submission    submitted to the EMBL Data Library, February 1993
#accession     S37483
#status        preliminary
#molecule_type mRNA
#residues      1-469 ##label DUC
#cross-references EMBL:X70423; NID:940625; PID:9406253
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
              immunoglobulin
KEYWORDS       immunoglobulin
FEATURE        276-345
SUMMARY        #domain immunoglobulin homology #label IG62
              #length 469 #molecular-weight 51349 #checksum 7833

Query Match          69.8%; Score 774; DB 2; Length 469;
Best Local Similarity 72.5%; Pred. No. 1.37e-104;
Matches 108; Conservative 22; Mismatches 17; Indels 2; Gaps 1;
```

```
RESULT          4
ENTRY          PL0011      #type fragment
TITLE          Ig heavy chain precursor V region (4C11) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
              18-Oct-1996
ACCESSIONS     PL0011
REFERENCE       PL0011
AUTHORS        Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;
              Kohler, H.
#journal        Mol. Immunol. (1988) 25:33-40
#title          Structural basis of stimulatory anti-idiotypic antibodies.
#cross-references MUID:88142863
#accession     PL0011
#molecule_type mRNA
#residues      1-151 ##label CHE
#experimental_source cell line 4C11
COMMENT         This protein is an anti-idiotypic antibody that induces an
              anti-phosphorylcholine response.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
              heterotetramer; immunoglobulin
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-19
              20-136
              50-54      #domain signal sequence #status predicted #label SIG\
              69-85      #product Ig heavy chain V region 4C11 #status predicted
              118-125     #region complementarity-determining 1\
              137-151     #region complementarity-determining 2\
              #domain C region (fragment) #status predicted #label COR
SUMMARY        #length 151 #checksum 2479

Query Match          69.2%; Score 767; DB 2; Length 151;
Best Local Similarity 70.3%; Pred. No. 2.00e-103;
Matches 104; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

DB 4 SWIFFLISGTRAGVISEVQLOOSGPELVNPGASVSKSCASGYTFTYVHWKQSHGS 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 4 SWVFLFLITTVGSQAYLOOSGAEIVRSASVSKSCASGYTFTYVHWKQTPGOG 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 LEWIGFPPNDNFENKFKDKATLTVDKSTTAYVMELSLTSEDSAYVCARDY-GA 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 64 LEWIGNIFPNGNDTYVNOFKKASLTADTSSSTAYVMOISLTSEDSAYVFCARG-N 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 IDYWGQGTSVTVSSAKTTPPSYPLAPG 150
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 124 IDYWGQGTSVTVSSAKTTPPYVPLVPG 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT          5
ENTRY          PN0444      #type fragment
TITLE          Ig heavy chain V region precursor - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              16-Aug-1996
ACCESSIONS     PN0444
REFERENCE       PN0444
AUTHORS        Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle,
              U.H.
#journal        Gene (1992) 122:321-328
#title          A general method for chimerization of monoclonal antibodies
              by inverse polymerase chain reaction which conserves
              authentic N-terminal sequences.
#accession     PN0444
#molecule_type mRNA
#residues      1-150 ##label KAL
#cross-references GB:I03346
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
              heterotetramer; immunoglobulin
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-19
              20-150
              #domain signal sequence #status predicted #label SIG\
              #product Ig heavy chain V region #status predicted
```

20-117 #label MAT\ #domain variable region #label VRG
SUMMARY #length 150 #checksum 9720

Query Match 68.8%; Score 763; DB 2; Length 150;
Best Local Similarity 69.3%; Pred. No. 9,216-103;
Matches 104; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

Db 1 MEMSWIFLLSLGAGVSEVLOQFGAEVYKPGTSVYKSCASGYITTDYNDMVKOSH 60
QY 1 MECWVFLFLSLITGVHSAVYLOQSGAEVRSKASGYITLTSYNMHWKQTP 60
Db 61 GKSLEWIDIDPNFDSSTYKFKGATLVKDSNTAYMELRSTSDTAIVYCARGCF 120
QY 61 GOGLEMINIRPGNDTYTNOKFKKASLTADTSSITAYMOISLTSDESAVYFCARGNW 120
Db 121 PYGMDYWGQSTSVYSSAKTTPPYPLAP 150
QY 121 EGALDYWGQSTSVYSSAKTTPPYPLVP 150

ENTRY 6
TITLE PS0024 #type complete
ORGANISM Ig heavy chain precursor V region (6A4) - mouse
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996

ACCESSIONS PS0024
REFERENCE PS0023
#authors Margot, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.;
#journal Duchene, M.; Domdey, H.
#title Gene (1988) 74:335-345
#title Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas aeruginosa outer membrane protein I.
#cross-references aeruginosa
#accession PS0024
#molecule_type mRNA
#residues 1-139 #label MAR
#experimental_source strain BALB/c
COMMENT This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas aeruginosa lipoprotein 1.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin; pyroglyutamic acid
FEATURE
1-19 #domain signal sequence #status predicted #label SIG
20-139 #domain Ig heavy chain V region #status predicted #label IGV
-117 #domain immunoglobulin homology #label IMN
#modified_site pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
#length 139 #molecular_weight 15673 #checksum 3803

SUMMARY

Query Match 67.3%; Score 746; DB 2; Length 139;
Best Local Similarity 76.3%; Pred. No. 6,106-100; Indels 2; Gaps 1;
Matches 106; Conservative 15; Mismatches 16;

Db 1 MERHWIFLFSVAGVSHOVLOQSGAEVYKPGTSVYKSCASGYITTDYNDMVKOSH 60
QY 1 MECWVFLFLSLITGVHSAVYLOQSGAEVRSKASGYITLTSYNMHWKQTP 60
Db 61 GOGLEWIDIDPNFDSSTYKFKGATLVKDSNTAYMELRSTSDTAIVYCARGCF 120
QY 61 GOGLEWIDIDPNFDSSTYKFKGATLVKDSNTAYMELRSTSDTAIVYCARGCF 120
Db 121 PYGMDYWGQSTSVYSSAKTTPPYPLAP 150
QY 121 EGALDYWGQSTSVYSSAKTTPPYPLVP 150

ENTRY 7
TITLE PL0012 #type fragment
ORGANISM Ig heavy chain precursor V region (F6-3) - mouse (fragment)

ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996

ACCESSIONS PL0012
REFERENCE PL0011
#authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;
#journal Kohler, H.
#title Mol. Immunol. (1988) 25:33-40
#title Structural basis of stimulatory anti-idiotypic antibodies.
#cross-references murine
#accession PL0012
#molecule_type mRNA
#residues 1-166 #label CHE
#experimental_source cell line F6-3
COMMENT This protein is an anti-idiotypic antibody which induces an anti-phosphorylcholine response.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-32 #domain signal sequence #status predicted #label SIG
33-151 #product Ig heavy chain V region #status predicted #label MAT
63-67 #region complementarity-determining 1
82-98 #region complementarity-determining 2
131-140 #region complementarity-determining 3
152-166 #domain C region (fragment) #status predicted #label COR

SUMMARY #length 166 #checksum 5824

Query Match 66.9%; Score 742; DB 2; Length 166;
Best Local Similarity 68.5%; Pred. No. 2,816-99; Indels 1; Gaps 1;
Matches 102; Conservative 20; Mismatches 26;

Db 17 SWIFLFLSLGAGVSEVLOQSGAEVYKPGTSVYKSCASGYITTDYNDMVKOSH 76
QY 4 SWIFLFLSLITGVHSAVYLOQSGAEVRSKASGYITLTSYNMHWKQTPGCG 63
Db 77 LEWIGSTNPIDTYNENKRGATVVDKSSIVYQMLSTSEDAVYICAREGFGN 136
QY 64 LEWIGSTNPIDTYNENKRGATVVDKSSIVYQMLSTSEDAVYICAREGFGN 136
Db 137 SLDYWGQSTSVYSSAKTTPPYPLAP 165
QY 123 ALDYWGQSTSVYSSAKTTPPYPLVP 151

ENTRY 8
TITLE H32513 #type complete
ORGANISM Ig heavy chain precursor V region (BXW16) - mouse
DATE 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998

ACCESSIONS H32513
REFERENCE A94689
#authors Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
#journal Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.
#journal J. Clin. Invest. (1988) 82:852-860
#title Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.
#cross-references murine
#accession H32513
#molecule_type DNA
#residues 1-137 #label KOF
#experimental_source strain BXW16
COMMENT This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas aeruginosa lipoprotein 1.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-137 #domain signal sequence #status predicted #label SIG
138-269 #domain Ig heavy chain V region #status predicted #label IGV
-117 #domain immunoglobulin homology #label IMN
#modified_site pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
#length 137 #molecular_weight 15108 #checksum 816

SUMMARY

Query Match 65.6%; Score 727; DB 2; Length 137;
Best Local Similarity 73.1%; Pred. No. 8,576-97; Indels 0; Gaps 0;
Matches 98; Conservative 22; Mismatches 14;


```

Db      120  YMGGISTVTSAAKTPPSYPLAPCS 146
      |||||||
Oy      126  YMGGISTVTSAAKTPPPVPLVPDS 152

RESULT  12
ENTRY   12
TITLE   HVMG7      #type complete
ORGANISM Ig heavy chain precursor V region (93G7, 36-65) - mouse
DATE     #formal_name Mus musculus #common_name house mouse
        18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change
        20-Mar-1998
ACCESSIONS A94264; A91261; A02028
REFERENCE   A94264
#authors   Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker,
#journal   P.W.; Capra, J.D.
#title     Science (1982) 216:309-311
#note      Somatic mutation in genes for the variable portion of the
#cross-references MIMD:82152818
#accession A94264
#molecule_type mRNA
#residues  1-140 #label SIM
#cross-references GB:J04933; NID:q195006; PID:q195007
#experimental_source strain A/J, hybridoma 93G7

REFERENCE A91261
#authors   Sleehartz, M.; Gefer, M.L.; Brodeur, P.; Riblet, R.;
#journal   Eur. J. Immunol. (1982) 12:1023-1032
#title     The genetic basis of antibody production: the dominant
#note      anti-arsenate idiotype response of the strain A mouse.
#cross-references MIMD:83131846
#accession A91261
#molecule_type DNA
#residues  20-76, 'TK', '79-118', 'V', '120-125', 'V', '127-134', 'T', '136-140
#label     #label SIM
#cross-references GB:M19292; NID:q196201; PID:q196202
#experimental_source strain A/J, hybridoma 36-65
#note      The sequence was determined from the differentiated gene
#note      from analysis of the sizes of several other
#note      differentiated genes that hybridize to this one, the
#note      authors conclude that all of these V regions have
#note      rearranged to the same J segment, JH2

GENETICS  16/1
#introns  1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; hybridoma; immunoglobulin
FEATURE    19
          140
          34-117 #domain signal sequence #status predicted #label SIG\
          41-115 #product Ig heavy chain V region (93G7) #status
          SUMMARY #domain immunoglobulin homology #label IMM\
                  #disulfide_bonds #status predicted
                  #length 140 #molecular_weight 15514 #checksum 6215

Query Match  63.9%: Score 709; DB 1; Length 140;
Best Local Similarity 73.0%: Pred. No. 8.15e-94;
Matches 100; Conservative 19; Mismatches 15; Indels 3; Gaps 2;

Db      4  SFTFLFLSTAGVHSEVLOQSGAEIYVRAGSSVYKMSCASGTYTTSYIGIMNVKQRPQG 63
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy      4  SWVELFLSTITGGHSAVYLDQSGAEIYVRGASGVYKMSCASGTYTTSYIMHNVKQTPQG 63

Db      64  LEWIGYINPGNGYINVEKFKTKTTLVDKSSSTAYMOLRSLTSEDSAYVEFCARSHYGG 123
      |||||  |||||  |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy      64  LEWIGNIFPENGDIYVQKFKKASLTADISSSTAIQMQLSSLTSEDSAYVEFCARQNW-EG 122

Db      124 SYDEYDWGGGTPLTVSS 140
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy      123 A-LDYWGQGTSTVTVSS 137

RESULT  13
ENTRY   S21810      #type complete

```

```

TITLE      Ig heavy chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE        20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
              08-Sep-1997

ACCESSIONS S21810
REFERENCE   S21810
            #authors Ostermeyer, M.; Brack, C.H.; Trautnacker, A.; Koehler, G.
            #submission submitted to the EMBL Data Library, January 1991
            #description Nucleotide sequence of a rearranged VDJ-region of a mouse Ig
                          mu heavy chain gene and its upstream region.
                          S21810

#accession S21810
#stratus   Preliminary
#molecule_type DNA
#residues  1-138 ##label OST
#cross-references EMBL:X56936; NID:g54163; PID:g54164

GENETICS   #introns 15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE      34-117
SUMMARY      #domain immunoglobulin homology #label IMM
              #length 138 #molecular-weight 15258 #checksum 1535

Query Match      63.8%; Score 708; DB 2; Length 138;
Best Local Similarity 74.1%; Pred. No. 1,19e-93;
Matches 100; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

Db 4 SRIFPLSTIAACVHOVOLOOSGPELVKPGASVHISCKASGFTPTSYIHVMVKORPGG 63
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 4 SWFFFLSLSTTVHSHQATLOOSGALVNSGASVMSCKASGYTLTSTNMHWKOTPEQG 63
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 64 LEWIGWIPGNTVNTKYNEKFKATLTADKSSSTAYMOLSLTSDSAVYFCARNGSSY 123
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
QY 64 LEWIGNIFPGNGDTYVNOKFKKASLTADTSSSTAYMQLSSTSDSAVYFCARNGMEG- 122
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 124 GLAYWOGTLYVYSA 138
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
QY 123 ALDYWGOGTSTVYSS 137
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT      14
ENTRY        PH1482
TITLE        Ig heavy chain V region (clones 36-351TG) and X7-TG) - mouse
              (fragment)
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
              16-Aug-1996
ACCESSIONS   PH1482; PH1495
REFERENCE     PH1482
            #authors Justiz, A.M.; Manser, T.
            #journal J. Exp. Med. (1993) 177:797-809
            #title Hypermutation is observed only in antibody H chain V region
                    Transgenes that have recombined with endogenous
                    immunoglobulin H DNA: Implications for the location of
                    cis-acting elements required for somatic mutation.
                    PH1482

#accession PH1482
#status     translation not shown
#molecule_type mRNA
#residues   1-140 ##label GTU
#experimental_source hybridoma cell

GENETICS     #introns 16/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE      34-117
SUMMARY      #domain immunoglobulin homology #label IMM
              #length 140 #checksum 6778

Query Match      63.6%; Score 705; DB 2; Length 140;
Best Local Similarity 73.7%; Pred. No. 3.74e-93;
Matches 101; Conservative 18; Mismatches 15; Indels 3; Gaps 2;

```

MUSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mparch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 15 17:57:49 1999; Maspar time 8.66 Seconds
627.099 Million cell updates/sec
at output not generated.

Title: >US-08-836-455-2
Description: (1-145) from US08836455.pep
Perfect Score: 1019
Sequence: 1 MGAPAQILGFLLLFPCTRC.....IKRADAPVTSIFPPSKRG 145

Scoring table: PAM 150
Gap 11
116695 segs, 37453910 residues

Searched: Minimum Match 0%
Post-processing: Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.409; Variance 104.536; scale 0.406

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description	Pred. No.
1	838	82.2	130	1	KVMSM4	Ig kappa chain precur	7.84e-116
2	690	67.7	106	2	PL0260	Ig kappa chain V regi	4.05e-91
3	688	67.5	106	2	PL0259	Ig kappa chain V regi	8.65e-91
4	686	67.3	234	2	SL4237	Ig kappa chain precur	1.87e-90
5	670	65.8	129	2	D32513	Ig kappa chain precur	8.40e-88
6	647	63.5	106	2	PL0262	Ig kappa chain precur	5.39e-84
7	645	63.3	117	1	KVMSB	Ig kappa chain V regi	1.15e-83
8	640	62.8	234	2	S01320	Ig kappa chain precur	7.74e-83
9	632	62.0	129	2	S40369	Ig kappa chain precur	1.62e-81
10	622	61.0	135	2	S40353	Ig kappa chain - huma	7.25e-80
11	622	61.0	141	2	S40354	Ig kappa chain V-J-C	7.25e-80
12	619	60.7	230	2	S33161	Ig kappa chain V-1 re	2.26e-79
13	615	60.4	123	2	S40313	Ig kappa chain V-J re	1.03e-78
14	615	60.4	129	2	B23986	Ig kappa chain precur	1.03e-78
15	614	60.3	98	2	PH1062	Ig kappa chain V regi	1.51e-78
16	614	60.3	108	4	B47271	nitrophenyl phosphon	1.51e-78
17	612	60.1	128	2	A26406	Ig kappa chain V regi	3.23e-78
18	610	59.9	129	2	S40317	Ig kappa chain - huma	6.89e-78
19	609	59.8	132	2	S40314	Ig kappa chain - huma	1.01e-77
20	607	59.6	127	2	PH1224	Ig kappa chain precur	2.15e-77
21	601	59.0	125	2	S40349	Ig kappa chain V-J re	2.09e-76
22	599	58.8	127	2	S52447	Ig kappa chain V regi	4.45e-76
23	598	58.7	130	2	S40368	Ig kappa chain - huma	6.50e-76

24	596	58.5	126	2	A34904	Ig kappa chain precur	1.39e-75
25	589	57.8	135	2	S24320	Ig kappa chain precur	1.96e-74
26	588	57.7	125	2	S40315	Ig kappa chain - huma	2.86e-74
27	588	57.7	127	2	S40367	Ig kappa chain V-J-C	2.86e-74
28	586	57.5	122	2	A29380	Ig kappa chain precur	6.10e-74
29	586	57.5	125	2	S40333	Ig kappa chain V-J re	6.10e-74
30	584	57.3	131	2	S40352	Ig kappa chain V-J-C	1.30e-73
31	583	57.2	115	2	UL0080	Ig kappa chain precur	1.90e-73
32	583	57.2	129	2	S52792	Ig kappa chain V regi	1.90e-73
33	583	57.2	129	2	S52789	Ig kappa chain V regi	1.90e-73
34	583	57.2	139	2	S40365	Ig kappa chain - huma	1.90e-73
35	582	57.1	126	2	S40335	Ig kappa chain V-J-C	2.77e-73
36	581	57.0	128	1	KVMS11	Ig kappa chain precur	4.04e-73
37	580	56.9	88	2	PL0261	Ig kappa chain V regi	5.89e-73
38	580	56.9	129	2	S40332	Ig kappa chain - huma	5.89e-73
39	579	56.8	128	2	S46372	Ig kappa chain variab	8.60e-73
40	578	56.7	128	2	PL0101	Ig kappa chain precur	1.25e-72
41	576	56.5	132	2	S38646	Ig kappa chain V regi	2.67e-72
42	574	56.3	101	2	B28840	Ig kappa chain V regi	5.68e-72
43	574	56.3	127	2	S11240	Ig kappa chain V regi	5.68e-72
44	573	56.2	101	2	C28840	Ig kappa chain V regi	8.29e-72
45	571	56.0	123	2	S40331	Ig kappa chain - huma	1.76e-71

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE KVMSM4 #type complete
CONTAINS Ig kappa chain precursor V region (MOPC 41) - mouse
ORGANISM Ig kappa chain precursor V region VK41
#formal_name Mus musculus #common_name house mouse
DATE 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996

ACCESSIONS
REFERENCE A93211; A93815; A94239; A01922; A01923
A93211
#authors Seidman, J.G.; Max, E.E.; Leder, P.
#journal Nature (1979) 280:370-375
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
#cross-references MOPC:79221900
#accession A93211
#molecule_type DNA
#residues 1-130 #label PC41
#accession B93211
#molecule_type DNA
#residues 1-117 #label VK41
#note the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41

REFERENCE
#authors Birstein, Y.; Schechter, I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.
#cross-references MOPC:77148916
#accession A93815
#molecule_type protein
#residues 1-33 #label BUR
#note Met-3 is apparently used as an alternative initiator in 25% of the chains

REFERENCE
#authors Gray, W.R.; Dreyer, W.J.; Hood, L.
#journal Science (1967) 155:465-467
#title Mechanism of antibody synthesis: size differences between mouse kappa chains.
#cross-references MOPC:67056897
#accession A94239
#molecule_type protein
#residues 23-49, 'B', '51-53', 'LSB', '57-58', 'zz', '61-62', 'B2', '65-76', 'B', '78-108, 110-130 #label GRA
#experimental_source Bence Jones protein MOPC 41

GENETICS
#introns 19/1

COMPLEX

An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

KEYWORDS #superfamily immunoglobulin V region; immunoglobulin heterotetramer; heterotetramer; immunoglobulin

FEATURE

1-22 #domain signal sequence #status experimental #label SIG1

3-22 #domain signal sequence #status experimental #label SIG2

23-130 #product Ig kappa chain V region (MORC 41) #status experimental #label M41

36-112 #domain immunoglobulin homology #label IMX

45-110 #disulfide-bonds #status predicted

SUMMARY #length 130 #molecular-weight 14311 #checksum 6707

Query Match 82.2%; Score 838; DB 1; Length 130;
Best Local Similarity 92.2%; Pred. No. 7.84e-116;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 3 MRAPQIFGFLLLFGQTRCDIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGP 62
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 1 MGPAPQIGFLLLFPQTRCDIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGP 60
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Db 63 DGTIKRLIYATSSLDGVPKRRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGG 122
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 61 DGTIKRLIYATSSLDGVPKRRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGG 120
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Db 123 GTRKEIKR 130
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 121 GTRKEIKR 128
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

RESULT 2
ENTRY PL0260 #type fragment
TITLE Ig kappa chain V region (anti-DNA, DP7YK) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
ACCESSIONS PL0260
REFERENCE #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, J. Exp. Med. (1990) 171:265-297
#journal D.; Marshak-Rothstein, A.; Weigert, M.
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.
#cross-references MUID:90111618
#accession PL0260
#molecule_type mRNA
#residues 1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

KEYWORDS #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

FEATURE

1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

SUMMARY #length 106 #checksum 2157

Query Match 67.7%; Score 690; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 4.05e-91;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGPDTIKRLIYATSSLDGVPK 60
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 21 DIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGPDTIKRLIYATSSLDGVPK 80
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Db 61 PRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGGTRKEI 106
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 81 PRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGGTRKEI 126
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

RESULT 3
ENTRY PL0259 #type fragment
TITLE Ig kappa chain V region (anti-DNA, DP1YK) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
ACCESSIONS PL0259
REFERENCE #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, J. Exp. Med. (1990) 171:265-297
#journal D.; Marshak-Rothstein, A.; Weigert, M.
#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.
#cross-references MUID:90111618
#accession PL0259
#molecule_type mRNA
#residues 1-106 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

KEYWORDS #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

FEATURE

1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

SUMMARY #length 106 #checksum 2162

Query Match 67.5%; Score 688; DB 2; Length 106;
Best Local Similarity 92.5%; Pred. No. 8.69e-91;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGPDTIKRLIYATSSLDGVPK 60
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 21 DIQMTQSPSSLSASLGERSLTCRASQDGGSLNMLQGPDTIKRLIYATSSLDGVPK 80
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Db 61 PRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGGTRKEI 106
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

Qy 81 PRSGSRGSDYSLTISLSEDFVYICLQYASSPWTFGGTRKEI 126
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4

RESULT 4
ENTRY S14237 #type complete
TITLE Ig kappa chain precursor (15C5) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997
ACCESSIONS S14237
REFERENCE #authors Vandamme, A.M.; Bulens, F.; Bernat, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
#journal Eur. J. Biochem. (1990) 192:767-775
#title Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.
#cross-references MUID:91006173
#accession S14237
#molecule_type mRNA
#residues 1-234 #label VAN
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

KEYWORDS #superfamily immunoglobulin V region; immunoglobulin heterotetramer; immunoglobulin

FEATURE

1-234 #region framework 1\
235-349 #region complementarity-determining 1\
350-449 #region framework 2\
450-556 #region complementarity-determining 2\
557-664 #region framework 3\
665-772 #region complementarity-determining 3\
773-880 #region framework 4

SUMMARY #length 234 #molecular-weight 26087 #checksum 6000

Query Match 67.3%; Score 686; DB 2; Length 234;
Best Local Similarity 69.0%; Pred. No. 1.87e-90;
Matches 98; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

D	b		1	MRTPAQFLGLILMFPEIKCDIMKTOSPPSMVSLERTVTVCRAKSNODINSVLSTWIOOKP	60
O	y		1	MGAAPQLIGLILLFPETRCIDIOMTOSPSSLSASLDQRVSLTCRASQDGINLHMLWLOEP	60
D	b		61	GKSPTLIYRGNRLVAGVPSRFSGSGSDYSLTISLEEDVGYYCYARDYFEFFPGS	120
O	y		61	DGTLTKRLIVATSSLGSGVPKRFGSRSSGDYSLTISLSEDFVAAYCYQIYASSPYTTGG	120
D	b		121	GTRKEIRADAAPIVSIFPPSS	142
O	y		121	GTRKEIRADAAPIVSIFPPSS	142
R	E	S	5	D32513 #type complete	
E	N	T		Ig kappa chain precursor V region (BXMI6) - mouse	
O	R	A		#formal_name Mus musculus #common_name house mouse	
D	A	T		21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998	
A	C	C		D32513	
R	E	F		A94689	
O	R	A		Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,	
A	C	C		A.N.	
R	E	S		J. Clin. Invest. (1988) 82:852-860	
E	N	T		Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.	
O	R	A		#cross-references MUID:88313394	
D	A	T		#accession D32513	
A	C	C		#molecule_type DNA	
R	E	S		##residues 1-129 ##label KOE	
O	R	A		#cross-references GB:M20832; NID:g196941; PID:g196942	
D	A	T		CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin	
S	U	M		length 129 #molecular_weight 14057 #checksum 3457	
Q	U	E		Query Match	
E	N	T		Best Local Similarity 76.8%; Pred. No. 8,40e-88;	
O	R	A		Matches 96; Conservative 10; Mismatches 19; Indels 0; Gaps 0;	
D	b		5	APAQFLGLILMPFAGARCDIQMTOSPPSMVSGSLGRVSLSCASQIGRNLDMYQAKRG	64
O	y		3	APAQFLGLILLFPETRCIDIOMTOSPSSLSASLGQVSVSLTCRASQDGINLHMLWLOEPDG	62
D	b		65	TIKLLIYSTNLNLSGVPSRFSGSGSDYSLTISLSEDFADYICLRNAVYPYFGGT	124
O	y		63	TIKLLIATSSLGSGVPKRFGSRSSDYSLTISLSEDFVAYICYOLOAASPYPFGGT	122
D	b		125	KLEIK	129
O	y		123	KLEIK	127
R	E	S	6	PL0262 #type fragment	
E	N	T		Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)	
O	R	A		#formal_name Mus musculus #common_name house mouse	
D	A	T		16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996	
A	C	C		PL0262	
R	E	S		REFERENCE PL0231	
O	R	A		Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pisetsky,	
D	A	T		D.; Marshak-Rothstein, A.; Weigert, M.	
E	N	T		J. Exp. Med. (1990) 171:265-297	
O	R	A		Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.	
A	C	C		#cross-references MUID:90111618	
R	E	S		#accession PL0262	
O	R	A		##molecule_type mRNA	
D	A	T		##residues 1-106 ##label SHL	
E	N	T		CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin	

[illegible]

TITLE Ig kappa chain precursor - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 10-Sep-1997

ACCESSIONS S01320
REFERENCE S01320
#authors de Maessle, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.

#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.
#cross-references EMBL:X13187; NID:951784; PID:951785
#accession S01320
#molecule_type mRNA
#residues 1-234 #label DE1
#cross-references EMBL:X13187; NID:951785
#note this sequence was determined from the differentiated gene

FEATURES
1-20 heterotetramer; immunoglobulin
21-234 #domain signal sequence #status predicted #label SIG\ #product Ig kappa chain #status predicted #label MAT

SUMMARY #length 234 #molecular_weight 25920 #checksum 6431

Query Match 62.8%; Score 640; DB 2; Length 234;
Best Local Similarity 60.6%; Pred. No. 7,74e-83;
Matches 86; Conservative 28; Mismatches 28; Indels 0; Gaps 0;

Db 1 MSVPTQVGLLLMLDARCDIQMTQSPASLSVSGESVITTCRASENISNLAWYQOKQ 60
QY 1 MGAPAQILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQOEP 60

Db 61 GKSQQLVYATKLVDPVPSRFSGSGSTQYSLKINSIQSDPFSYTCQHWDPPTFGS 120
QY 61 DGTIKRLIYATSSLSGSGVPSRFSRSGSDYSLTISLSEDFVAYYCLQYASSPYTFGG 120

Db 121 GTKLEMRADAPTVSIFPPSS 142
QY 121 GTKLEIRADAPTVSIFPPSS 142

RESULT 9
ENTRY S40369 #type complete
TITLE Ig kappa chain - human
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
#formal_name Homo sapiens #common_name man
06-Mar-1994 #sequence_revision 26-May-1995 #text_change 08-Sep-1997

ACCESSIONS S40369
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.
#accession S40369
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-129 #label KIE
#cross-references EMBL:X72479; NID:9441426; PID:9441427
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 129 #molecular_weight 14063 #checksum 6277

Query Match 62.0%; Score 632; DB 2; Length 129;
Best Local Similarity 68.8%; Pred. No. 1.62e-81;
Matches 88; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

Db 2 MRVLAQLGLLCEPGARCDIQMTQSPSSLSASVGDRTVITCRASHYISNHLVWFOOKP 61
QY 1 MGAPAQILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQOEP 60

Db 62 GKAPKSLIYATSSLSGSGVPSRFSGSGSTQYSLKINSIQSDPFSYTCQHWDPPTFGS 121
QY 62 GKAPKSLIYATSSLSGSGVPSRFSGSGSTQYSLKINSIQSDPFSYTCQHWDPPTFGS 121

QY 61 DGTIKRLIYATSSLSGSGVPSRFSRSGSDYSLTISLSEDFVAYYCLQYASSPYTFGG 120
Db 122 GTKLEIR 129
QY 121 GTKLEIR 128

RESULT 10
ENTRY S40353 #type complete
TITLE Ig kappa chain V-J-C region - human
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
DATE 19-May-1994 #sequence_revision 26-May-1995 #text_change 20-Mar-1998

ACCESSIONS S40353
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their hypermutation.
#accession S40353
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-125 #label KIE
#cross-references EMBL:X72463
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 125 #molecular_weight 13441 #checksum 9514

Query Match 61.0%; Score 622; DB 2; Length 125;
Best Local Similarity 68.3%; Pred. No. 7.25e-80;
Matches 84; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

Db 1 LUGLLIMFPGARCDIQMTQSPSSLSASVGDRTVITCRASQIGNDLGWYQKRPAPKR 60
QY 7 ILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQOEPDGTIKR 66

Db 61 LIYATSSLSGSGVPSRFSGSGSTQYSLKINSIQSDPFSYTCQHWDPPTFGS 120
QY 67 LIYATSSLSGSGVPSRFSRSGSDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLET 126

Db 121 KRT 123
QY 127 KRA 129

RESULT 11
ENTRY A49134 #type fragment
TITLE Ig kappa chain V-I region (ISE) - human (fragment)
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Sep-1997

ACCESSIONS A49134
REFERENCE A49134
#authors Rocca, A.; Khamilich, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.; Cogné, M.
#journal Clin. Exp. Immunol. (1993) 91:506-509
#title Primary structure of a variable region of the V kappa I subgroup (ISE) in light chain deposition disease.
#cross-references EMBL:93185310
#accession A49134
#status preliminary
#molecule_type mRNA; protein
#residues 1-141 #label ROC
#cross-references EMBL:X67322; NID:933268; PID:933269
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 141 #checksum 3566

Query Match 61.0%; Score 622; DB 2; Length 141;
Best Local Similarity 61.2%; Pred. No. 7.25e-80;
Matches 85; Conservative 28; Mismatches 26; Indels 0; Gaps 0;

Db	1	AQLIGLILFFPARCDIQMTQSPSSLSASVDVRYITCRASQGIKRNDAWFOQKPKAP	60
QY	5	AQLIGLILFFPRTRODQIMQSPSSLSASLQGRVSLTCRASQDIGINLHWLQGPDDTI	64
Db	61	KRLIYDASLSLGSVPRFSGSGGTEFTLTITSSLDPEDFAYIYCLQYNGYPRTEGQTKV	120
QY	65	KRLIYATSSLSGSGVPRFSGSGSGSYSLTISLSEDFVAYICLQYASSPYTFGCGTKL	124
Db	121	EIK 123	
QY	125	EIK 127	
RESULT	14		
ENTRY			
TITLE	B23986	#type complete	
ORGANISM	Ig kappa chain precursor V region (IR2) - rat		
DATE	17-Sep-1987	#formal_name Rattus norvegicus #common_name Norway rat	
	16-Aug-1996	#sequence_revision 17-Sep-1987 #text_change	
ACCESSIONS	B23986		
REFERENCE	A91541		
#authors	Heliman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.		
#journal	Gene (1985) 40:107-114		
#title	Structure and expression of kappa-chain genes in two		
	IgE-producing rat immunocytomas.		
#cross-references	MJID:86137406		
#accession	B23986		
	#molecule_type mRNA		
CLASSIFICATION	#residues 1-129	#label HEL	
KEYWORDS	#superfamily immunoglobulin V region; immunoglobulin homology		
SUMMARY	heteroleptamer; immunoglobulin		
	#length 129 #molecular-weight 14217 #checksum 5336		
Query Match			
Best Local Similarity	60.4%; Score 615; DB 2; Length 129;		
Matches	84; Conservative 20; Mismatches 23; Indels 0; Gaps 0;		
Db	3	MRAHQFLGLIMCFGARGCDIQMTQSPSSSVSLGDTVITPCRASQDVGYIVIFQCKP	62
QY	1	MGAPAQGLGLLFLFPETRCDIQMTQSPSSLSASLQGRVSLTCRASQDIGINLHWLQGP	60
Db	63	GKSPRLIYATTLADGVPFRFSGSGSDYSLTISLSEEDVADYHCLQYKNEYTFGP	122
QY	61	DGTRKRLIYATSSLGSVPRFSGSGSDYSLTISLSEDFVAYIYCLQYASSPYTFGG	120
Db	123	GTKLEIK 129	
QY	121	GTKLEIK 127	
RESULT	15		
ENTRY			
TITLE	PH1062	#type fragment	
ORGANISM	Ig light chain V region (clone 202.105) - mouse (fragment)		
DATE	30-Sep-1993	#formal_name Mus musculus #common_name mouse	
	15-Jun-1996	#sequence_revision 30-Sep-1993 #text_change	
ACCESSIONS	PH1062		
REFERENCE	PH0971		
#authors	Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.		
#journal	J. Exp. Med. (1992) 176:761-779		
#title	Both IgM and IgG anti-DNA antibodies are the products of		
	clonally selective B cell stimulation in (NZB x NZW)F1		
	mice.		
#accession	PH1062		
#status	nucleic acid sequence not shown		
#molecule_type	mRNA		
#residues	1-98	#label TIL	
#experimental_source	B cell, strain [NZB x NZW]F1		
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology		
KEYWORDS	immunoglobulin		

SUMMARY #length 98 #checksum 6933

Query Match 60.38; Score 614; DB 2; Length 98;
Best Local Similarity 87.88; Pred. No. 1.5le-78;
Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASLGKRVSLTCRASQEIISGYLWLGQKPDGTIKRLIYSTSTLNSGVPR 60
|||||+|||||:|||||:| ||| |||||||:| ||||
QY 21 DIQMTQSPSSLSASLGKRVSLTCRASQDIGINLHWLQKPEDGTIKRLIYATSSLSGSGVPR 80
Db 61 RPSGSRSGSDYSLTISLSEDFADYCYCLOYASSPYTF 98
|||||+|||||:|||||:| ||| |||||||:| ||||
QY 81 RPSGSRSGSDYSLTISLSEDFVAYCYCLOYASSPYTF 118

Search completed: Thu Apr 15 17:58:14 1999
Job time : 25 secs.

CC diagnostic kits and methods of using J1D10, J1D10 polypeptides
CC and/or J1D10 polynucleotides, including methods of treating HMG-
CC associated tumors.
SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T;

Query Match 100.0%; Score 435; DB 34; Length 435;
Best Local Similarity 100.0%; Pred. No. 2,086-293;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 atgggggccccctgcctcagatcttcgggtcttctgtcttctgtttccagggtaccagatgt 60
|||
QY 1 ATGGGGGCCCCCTGCTCAGATCTTGGGTTCTGTGCTCTTCCAGGTACAGATGT 60
|||
Db 61 gacatccagatgacccagctccatccctctctctcgtctctcgggaagaagaagtaagt 120
|||
QY 61 GACATCCAGATGACCCAGCTCCATCTCTTATCTGCTCTGCGGACAAAGATCAGT 120
|||
Db 121 ctcaactgtcggcgaagtcagagacattglatlaactacatcagcttcagcagaagaca 180
|||
QY 121 CTCACCTGTGCGGCAAGTCAGACATTTGTTAACTTACCTTGGCTTCACAGAACCA 180
|||
Db 181 gatggaactataaagcctctatctacgcacatccagtttagttctgtgtcccaaa 240
|||
QY 181 GATGGAACATAAAGCCCTGATCTACGCCACATCCAGTTAGGTTGCGTCCCAAA 240
|||
Db 241 aggttcagtgccagtagtctggttcagattatctctccaccatcagagccttgatct 300
|||
QY 241 AGGTTCAAGTGCATAGTCTGCGGTGAGATTTCTTCACATCAGACGCTTGAGCT 300
|||
Db 301 gaagattttgagcctatctactgtctacaatatgtagtctccgtacagcttcgagag 360
|||
QY 301 GAAGATTTTGTAGCCTATTACTGTCTCAATATGCTAGTTCTCGGTACAGCTTGAGAGG 360
|||
Db 361 gggaaccaagcttggaataaagggtgtagtctgcacccaactgtatcatctccacca 420
|||
QY 361 GGGACCAAGCTGGAAATAAAGGGGTGATGCTGCACCAACTGTATCATCTCCACCA 420
|||
Db 421 tccagtaagcttggg 435
|||
QY 421 TCCAGTAAGCTTTGGG 435
|||

RESULT 2
ID N30165 standard; DNA; 450 BP.
AC N30165:

DT 25-MAR-1992 (first entry)
Sequence encoding the leader, variable region and first 16 AAs of
the constant region of the kappa-chain (light chain) of MOPC41.

DIagnosis; therapy; immunoglobulin; ss.
OS Homo sapiens.

PH Key Location/Qualifiers
FT cds 13..78
FT /*tag= a
FT /product= leader
FT 79..402
FT /*tag= b
FT /product= variable region
FT 403..450
FT /*tag= c
FT /product= constant region

EP-88994-A.
PD 21-SEP-1983.
PF 10-MAR-1983; 001655.
PR 15-MAR-1982; US-338414.
PR 05-DEC-1983; US-558551.
PA (SCHE) SCHERING CORP.
PA (DNAX-) DNAX RES INST.
PI Moore KW, Zaffaroni A;
DR WPI; 83-772290/39.
DR P-PSDB; P30251.
PT Transformed expression vectors or plasmid(s) - with double
PT stranded DNA sequence coding only for desired part of polypeptide
PT chain

PS Example: Page 40-41; 68pp; English.

CC The pref. vector or plasmid of the invention has a double-stranded
CC DNA seq. coding for a variable region of a light or heavy chain of
CC IgG, or for a variable region of a light or heavy chain of an
CC immunoglobulin specific for an enzyme or surface protein. The
CC sequence esp. codes for a variable region of a light chain having 95-
CC 115 AAs or for a variable region of a heavy chain having 110-125 AAs
CC esp. including the D region of the heavy chain.
SQ Sequence 450 BP; 108 A; 114 C; 104 G; 124 T;

Query Match 88.7%; Score 386; DB 4; Length 450;
Best Local Similarity 94.9%; Pred. No. 2,456-257;
Matches 408; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 19 atgagggctctcagacagatttgcttctgtcttctgttcttcaagggtaccagatgt 78
|||
QY 1 ATGGGGGCCCCCTGCTCAGATCTTGGGTTCTGTGCTCTTCCAGGTACAGATGT 60
|||
Db 79 gacatccagatgacccagctccatccctctctctctcgtctctcgggaagaagaagtaagt 138
|||
QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTGCGGACAAAGATCAGT 120
|||
Db 139 ctcaactgtcggcgaagtcagagacattgtagtagcttaactggtctcagcagaagaca 198
|||
QY 121 CTCACCTGTGCGGCAAGTCAGACATTTGTTAACTTACCTTGGCTTCAGAGAACCA 180
|||
Db 199 gatggaactataaagcctctatctacgcacatccagtttagattctgtgtcccaaa 258
|||
QY 181 GATGGAACATAAAGCCCTGATCTACGCCACATCCAGTTAGGTTCTGCTGCCCAAA 240
|||
Db 259 aggttcagtgccagtagtctggttcagattatctctccaccatcagagccttgatct 318
|||
QY 241 AGGTTCAAGTGCATAGTCTGCGGTGAGATTTCTTCACATCAGACGCTTGAGCT 300
|||
Db 319 gaagattttgagcctatctactgtctacaatatgtagtctccgttcgtagagtcgtg 378
|||
QY 301 GAAGATTTTGTAGCCTATTACTGTCTCAATATGCTAGTTCTCGGTACAGCTTGAGAGG 360
|||
Db 379 ggcaaccaagcttggaataaagggtgtagtctgcacccaactgtatcatctccacca 438
|||
QY 361 GGGACCAAGCTGGAAATAAAGGGGTGATGCTGCACCAACTGTATCATCTCCACCA 420
|||
Db 439 tccagtaggc 448
|||
QY 421 TCCAGTAAGC 430
|||

RESULT 3
ID T77851 standard; CDNA; 387 BP.
AC T77851:

DT 03-NOV-1997 (first entry)
DE Murine anti-human Class II monoclonal antibody 44H104 VL chain CDNA.
KW Antibody; light chain; variable region; hybridoma cell line 44H104;
KW Immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW antigen delivery; ss.

OS Mus musculus.
PH Key Location/Qualifiers
FT cds 1..387
FT /*tag= a
FT /note= "Encodes 44H104 light chain variable region,
FT including secretion signal; termination
FT codon not given"

PN W09640941-A1.
PD 19-DEC-1996.
PF 07-JUN-1996; CA0400.
PR 07-JUN-1995; US-483576.
PA (CONN-) CONNAUGHT LAB LTD.
PI Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
DR WPI; 97-077271/07.
DR P-PSDB; W22537.
PT Recombinant conjugate antibody mol., modified for delivering an
PT antigen - elicits enhanced immune response without the use of
PT adjuvant to generate antibodies which are useful in vaccines or

PT Immuno:diagnosis
 CC Example 1: Fig 1A; 64pp; English.
 CC Novel recombinant conjugate antibody molecules comprise a monoclonal
 CC antibody specific for a surface structure of antigen presenting
 CC cells (APC), genetically modified to contain at least one antigen
 CC exclusively at one or more preselected sites. The conjugate is capable
 CC of delivering the antigen to APC and eliciting an immune response to
 CC the antigen. The new conjugates are useful as vaccines and are able
 CC to elicit an enhanced immune response without the use of an adjuvant.
 CC In a specific example, a conjugate was constructed using the murine
 CC anti-human class II monoclonal antibody secreted by hybridoma
 CC 44H104. The peptide CTRB36 was chosen as antigen; it consists of
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.
 CC The present sequence encodes the light chain variable region of a
 CC was PCR amplified from 44H104 and used in the preparation of a
 CC conjugate with antigen CTRB36.
 CC Sequence 387 BP; 90 A; 95 C; 90 G; 112 T;
 Query Match 71.0%; Score 309; DB 33; Length 387;
 Best Local Similarity 90.6%; Pred. No. 7,50e-201;
 Matches 345; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Db 7 atgaaggttcctcctcaagcttctgctctctgctgctgcttccaggtaccagatgt 66
 Qy 1 ATGGGGGCCCCCTCTCAGATTCTTGGTCTTGTCTGCTTGTTCAGGTACAGATG 60
 Db 67 gaatccagatgacagctccatctcctctctctctgctcctctctggacaagaatcagt 126
 Qy 61 GACATCCAGATGACCCAGTCCATCCTCTTATCTGCTCTGAGCAAAAGACAGT 120
 Db 127 ctcaactgttcggcaagtcaggaatattggttacttaacccgtgctcagcaagaacca 186
 Qy 121 CTCACCTTGCGGCAAGTACGACATTGTATTAATTAATTAATTAATTAATTAATTA 180
 Db 187 gatgaacattataacgcctgtgtctacgcgcgtcccaactttagattctggtgtcccaaa 246
 Qy 181 GATGGAACATTAATAACCCCTGATCTACGCCACATCCAGTTAGTCTGTGTCGCCCAA 240
 Db 247 aggttcagtgagcagtgatgctggtggtggtggtggtggtggtggtggtggtggtggt 306
 Qy 241 AGGTTAGTGCGGCAAGTACGCTGAGTATTAATTAATTAATTAATTAATTAATTAAT 300
 Db 307 gaagatttgcagactactactgtctacaaataataataataataataataataataata 366
 Qy 301 GAAGATTGTTAGACCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 Db 367 gggaccacagctggagctgaa 387
 Qy 361 GGGACCAAGCTGGAAATAAA 381
 RESULT 4
 ID 046084 standard; cDNA: 739 BP.
 AC 046084;
 DT 07-FEB-1994 (first entry)
 DE Sequence encoding 520C9 sfv protein.
 KW Single chain Fv polypeptide: VH-VL heterodimer; immunoglobulin; Ig;
 KM biosynthetic single polypeptide chain binding site; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT cds 1..739
 FT /tag= a
 PN MO9316185-A.
 PD 19-AUG-1993
 PF 05-FEB-1993; U01055.
 PR 06-FEB-1992; US-831967.
 PA (CETU) CETUS ONCOLOGY CORP.
 PI (CREA-) CREATIVE BIOMOLECULES INC.
 PI Houston IL, Huston JS, Oppermann H, Ring DB;
 DR WPI: 93-272889/34.
 DR P-PSDB: R39569.
 PT New single chain Fv polypeptide binding to C-erbB-2 tumour
 antigen - for imaging or treating breast or ovarian cancer etc.

PS Disclosure: pages 60-61; 87pp; English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells. Such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
 CC pt. of about 5.3 (see 046083, R39568). A single chain Fv (scFv)
 CC is a covalently linked VH-VL heterodimer which is expressed from
 CC a gene fusion including VH- and VL- encoding genes connected by
 CC a peptide-encoding linker. Such linker sequences are set forth in
 CC AA residues 116-135 in R39569, which includes part of the 16 AA
 CC linker sequences in R39572. Using 046084 for the 520C9 monoclonal
 CC antibody, a single chain polypeptide can be produced having a
 CC binding affinity for a C-erbB-2 related antigen.
 CC Sequence 739 BP; 188 A; 177 C; 181 G; 193 T;
 Query Match 69.7%; Score 303; DB 8; Length 739;
 Best Local Similarity 95.2%; Pred. No. 1.83e-196;
 Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 Db 395 gatccgatatccagatgacccagctccatctcctctctctctctctctgaggaagaag 454
 Qy 56 GATGTACATCCAGATGACCCAGTCCATCCTCTTATCTGCTCTGAGCAAAAGAG 115
 Db 455 tcagctcactgttcggcaagtcaggaatggaatggaatggaatggaatggaatggaatgga 514
 Qy 116 TCAGTCTCACTTGTGCGGCAAGTACGACATTGTTAACTTAATTAATTAATTAATTAAT 175
 Db 515 aaccagatggaactatlaaacgcctgatctacacacacacacacacacacacacacacac 574
 Qy 176 AACCAAGATGAACATTAATAACCCCTGATTAACGCCACATCAAGTTAGTTAGTTAGTTC 235
 Db 575 ccaaaagtcctgctgagcgtgctggtggtggtggtggtggtggtggtggtggtggtggt 634
 Qy 236 CCAAAAGTTCAGTGCACATAGTCTGCTGCTGATTAATTAATTAATTAATTAATTAAT 295
 Db 635 agctgaagatttttagctctactgtctacaaataataataataataataataataataata 694
 Qy 296 AGCTGCAAGATTTTGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 355
 Db 695 gaggggggacacactggaataaagggctgat 729
 Qy 356 GAGGGGGGACCAAGCTGGAAATAAAAGGGGCTGAT 390
 RESULT 5
 ID T36880 standard; cDNA: 739 BP.
 AC T36880;
 DT 29-OCT-1996 (first entry)
 DE 520C9 anti-C-erbB-2 two single chain Fv construct.
 KW 520C9; anti-C-erbB-2 monoclonal antibody; single chain Fv; sfv;
 KM construct; polypeptide linker; C-terminal amino acid sequence;
 KW in vivo imaging; drug targeting experiment; homodimer;
 OS increased; binding avidity; tissue retention time; ss.
 FH Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 1..732
 FT /note= "START codon absent"
 FT /tag= a
 PN US534254-A.
 PD 09-JUL-1996.
 PF 06-FEB-1992; 831967.
 PR 06-FEB-1992; US-831967.
 PR 07-OCT-1993; US-133804.
 PA (CHIR) CHIRON CORP.
 PI (CREA-) CREATIVE BIOMOLECULES INC.
 PI Houston IL, Huston JS, Oppermann H, Ring DB;
 DR WPI: 96-333194/33.
 DR P-PSDB: W02280.
 PT Compsns. congy. antigen-targetting antibody fragment constructs -
 PT comprising dimer of single-chain Fv fragments
 CC Example 1: Columns 33-36; 30pp; English.
 CC Variable heavy (VH) and variable light (VL) genes were cloned from
 CC a 520C9 hybridoma cDNA library, using probes directed toward the
 CC antibody constant and joining regions. A two single chain Fv (scFv)

CC gene was constructed by connecting the VH and VL genes with a
 CC Ser rich polypeptide linker. The resulting 520C9 two sfv gene, the
 CC present sequence, was inserted into an expression vector.
 CC transformed into E. coli, and protein expression induced by the
 CC addn. of IPTG to the culture medium.
 CC A compsn. comprising a carrier and the 2 sfv protein prod. can be
 CC used for in vivo imaging, and drug targeting experiments. The
 CC 2 sfv protein prod. is a homodimer, in which both fragments target
 CC the same antigen, therefore giving greater binding avidity and
 CC longer tissue retention times, compared to individual sfv protein
 CC prod. fragments.
 SQ Sequence 739 BP; 188 A; 177 C; 181 G; 193 T;

Query Match 69.7%; Score 303; DB 22; Length 739;
 Best Local Similarity 95.2%; Pred. No. 1.83e-196;
 Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 395 gatcgatataccagatgacagctgcacatcctctctatctgctctctggaggaagag 454
 56 GATGTCATCCAGATGACCCAGTCCTCATCTCTTATCTGCTCTCTGGACAAAGAG 115
 Db 455 tcaactcactgttcggcgaagtcagacatgtgtaataagcttaacctgcttcagcag 514
 116 TCAGTCTCACTGTGCGGCAAGTCAGACATGTGTAATTAACATTAGCTTCAGCAGG 175
 Db 515 aaccagatggaactatataagcctgatactacgacacatccagtttagttgtctc 574
 176 AACCGATGGAACATTAATTAACCCCTGATCTACGCCACATCCAGTTAGTGTGCTGTC 235
 Db 575 ccaaaaggttcagtcgagcgtgctggtgaatattcttcacatccagtagccttg 634
 236 CCAAAAGGTTCACTGTGCGGCAAGTCAGACATGTGTAATTAACATTAGCTTCAGCAGCCTTG 295
 Db 635 agtctgaagattttagtctatctactgcttacaatgctatcttccgtacacgttcg 694
 296 AGTCTGAAGATTTTGTAGCCTATTACTGTCATAATATCTAGTTCTCGTACAGCTTCG 355
 Db 695 gaggggggacccaacttggaataaacyggctgat 729
 356 GAGGGGGGACCAAGCTGGAATAAAGCGGCTGAT 390
 Qy 356 GAGGGGGGACCAAGCTGGAATAAAGCGGCTGAT 390

RESULT 6
 ID Q46086 standard; cDNA; 1605 BP.
 AC Q46086;
 DT 07-FEB-1994 (first entry)
 DE Sequence encoding G-FIT.
 OS Tumour antigen; c-erbB-2; G-FIT; ss.
 BC Synthetic.

FN Key Location/Qualifiers
 FT cds 1..1605
 FT WO9316185-A.
 PD 19-AUG-1993.
 PE 05-FEB-1993; U01055.
 PR 06-FEB-1992; US-831967.
 PA (CETUS) CETUS ONCOLOGY CORP.
 PI (CREA-) CREATIVE BIOMOLECULES INC.
 PI Houston IL, Houston JS, Oppermann H, Ring DB;
 DR WPI: 93-272889/34.
 DR P-PSDB: R395671.
 PT New single chain Fv polypeptide binding to C-erbB-2 tumour
 PT antigen - for imaging or treating breast or ovarian cancer etc.
 PT Example; pages 65-68; 87pp; English.
 CC c-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
 CC pt. of about 5.3 (see Q46083, R39568).
 SQ Sequence 1605 BP; 434 A; 354 C; 373 G; 444 T;

Query Match 67.4%; Score 293; DB 8; Length 1605;
 Best Local Similarity 93.7%; Pred. No. 3.73e-189;
 Matches 314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 1268 gatcgatataccagatgacagctgcacatcctctctatctgctctctggaggaagag 1327
 56 GATGTCATCCAGATGACCCAGTCCTCATCTCTTATCTGCTCTCTGGACAAAGAG 115
 Db 1328 tcaactcactgttcggcgaagtcagacatgtgtaataagcttaacctgcttcacag 1387
 116 TCAGTCTCACTGTGCGGCAAGTCAGACATGTGTAATTAACATTAGCTTCAGCAGG 175
 Db 1388 aaccagatggaactatataagcctgatactacgacacatccacttagattgtgtctc 1447
 176 AACCGATGGAACATTAATTAACCCCTGATCTACGCCACATCCAGTTAGTGTGCTGTC 235
 Db 1448 ccaaaaggttcagtcgagcgtgctggtgaatattcttcacatccagtagccttg 1507
 236 CCAAAAGGTTCACTGTGCGGCAAGTCAGACATGTGTAATTAACATTAGCTTCAGCAGCCTTG 295
 Db 1508 agtctgaagattttagtctatctactgcttacaatatactatttccgtacacgttcg 1567
 296 AGTCTGAAGATTTTGTAGCCTATTACTGTCATAATATCTAGTTCTCGTACAGCTTCG 355
 Qy 1568 gaggggggacccaacttggaataaacyggctgat 1602
 356 GAGGGGGGACCAAGCTGGAATAAAGCGGCTGAT 390

RESULT 7
 ID Q97507 standard; DNA; 321 BP.
 AC Q97507;
 DT 21-DEC-1995 (first entry)
 DE Light chain variable region for monoclonal antibody 5G4.
 KW Monoclonal antibody; heavy metal: mercury; variable region;
 KM Light chain; ss.
 OS Synthetic.
 FN Key Location/Qualifiers
 FT cds 1..321
 FT WO9520607-A.
 PD 03-AUG-1995.
 PE 27-JAN-1995; U01199.
 PR 27-JAN-1994; US-187407.
 PA (BION-) BIONEERASKA INC.
 PI Lopez O, Wagner FW, Wylie DE;
 DR WPI: 95-275415/36.
 DR P-PSDB: R97250.
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals
 PS Claim 2; Page 65-66; 106pp; English.
 CC Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
 CC 5B6 and 3E8) were producing MAbs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CHI domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' and of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in Q97511-Q97518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used
 CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer Q97518
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
 CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer Q97518
CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in Q97498-097510 and the deduced AA sequences in R79241-R79250 &
CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
SQ Sequence 321 BP; 82 A; 80 C; 72 G; 87 T;

Query Match 65.3%; Score 284; DB 15; Length 321;
Best Local Similarity 94.4%; Pred. No. 1,40e-182;
Matches 302; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1 gacatccagatgacccagctccatccctctatctcgtcctctctggagaagaagtcact 60
|||||
61 GACATCCAGATGACCCAGCTCCATCCTTATCTGCGCTCTGGAGACAAAGTCACT 120
|||||
62 ctcaactgtcggcgccagtcagagcattgtagttaaactgctcagctgaacca 120
|||||
121 CTCACCTTGCGGGCAGTACAGGACATTGGTATTAATTAATGCTTCAGCAGAACCA 180
|||||
122 gatggaactataaagcctgactcagccactcgggttttagattctggtcccaaa 180
|||||
181 GATGGAACTATTAAAGCCCTGATCTACGCCACATCCAGTTTGGTGTGCCCAA 240
|||||
182 aggttcagtcgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 240
|||||
241 AGGTTCAGTCGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 300
|||||
242 gaagatttgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
|||||
301 GAAGATTGTTGTAACCTTACTCTCTACATATGCTAGTTCTCGTACAGCTTCGAGG 360
|||||
302 gggaccaagctggaataaa 320
|||||
361 GGGACCAAGCTGGAATAAA 380
|||||

RESULT 10
ID 015114 standard; DNA: 432 BP.
AC 015113:
DT 16-MAR-1992 (first entry)
DE IL-2 chimeric antibody light chain clone 447.
KW Interleukin-2; immunosuppressant.
OS Chimeric Homo sapiens.
FH Chimeric Mus musculus.
FT cds 1..432 location/Qualifiers
FT signal_peptide 1..60 /tag= a
FT mat_peptide 61..432 /tag= b
FT EP-460674-A. /tag= c
PD 11-DEC-1991.
PF 06-JUN-1991; 109303.
PR 08-JUN-1990; DE-018442.
PA (BOE) BOEHRINGER MANNHEIM GMBH.
PI Weidle U, Kaluza B, Knapp W;
DR WPI: 91-363168/50.
P-PSDB: R15321.
PT New recombinant DNA encoding chimeric antibody - with human
PT constant and non-human variable regions, esp. directed against
PT interleukin 2 receptor
PS Disclosure: Page 11; 24pp; German.
CC The sequence encodes the interleukin-2 (IL-2) chimeric antibody light
CC chain clone 447. Antibodies against IL-2 receptors are useful as
CC immunosuppressants, and are much less immunogenic than mouse or
CC rat antibodies. The DNA sequence provides much higher yields of
CC chimeric antibodies than known methods. See also Q15114-Q15118.

SQ Sequence 432 BP; 106 A; 102 C; 104 G; 120 T;
Query Match 57.0%; Score 248; DB 3; Length 432;
Best Local Similarity 78.8%; Pred. No. 2.36e-156;
Matches 339; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Db 1 atgagtgctcttcgctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 60
|||||
111 ggg 120
|||||
121 atcaacttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180
|||||
181 ggggaatcattaaagggcctgactatcatcaggaaccaacttggaagaggtccatca 240
|||||
241 cggttcagtcgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
|||||
301 AGGTTCAGTCGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 360
|||||
302 gaagatttgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 360
|||||
361 GAAGATTGTTGTAACCTTACTCTCTACATATGCTAGTTCTCGTACAGCTTCGAGG 420
|||||
421 tccagtgagc 430
|||||
422 TCCAGTGAAC 430
|||||

RESULT 11
ID 015113 standard; DNA: 432 BP.
AC 015113:
DT 16-MAR-1992 (first entry)
DE IL-2 chimeric antibody light chain 179.
KW Interleukin-2; immunosuppressant.
OS Chimeric Homo sapiens.
FH Chimeric Mus musculus.
FT cds 1..432 location/Qualifiers
FT signal_peptide 1..60 /tag= a
FT mat_peptide 61..432 /tag= b
FT EP-460674-A. /tag= c
PD 11-DEC-1991.
PF 06-JUN-1991; 109303.
PR 08-JUN-1990; DE-018442.
PA (BOE) BOEHRINGER MANNHEIM GMBH.
PI Weidle U, Kaluza B, Knapp W;
DR WPI: 91-363168/50.
P-PSDB: R15321.
PT New recombinant DNA encoding chimeric antibody - with human
PT constant and non-human variable regions, esp. directed against
PT interleukin 2 receptor
PS Disclosure: Page 10; 24pp; German.
CC The sequence encodes the interleukin-2 (IL-2) chimeric antibody light
CC chain clone 179. Antibodies against IL-2 receptors are useful as
CC immunosuppressants, and are much less immunogenic than mouse or
CC rat antibodies. The DNA sequence provides much higher yields of
CC chimeric antibodies than known methods. See also Q15114-Q15118.
SQ Sequence 432 BP; 107 A; 101 C; 105 G; 119 T;

D	b8	gacataagatgaaccagctcccatcattccatgtatatgcattccttagagaagatcacag	141
Oy	61	GACATTCAGATGACCCTCATCCTCTTATTCTCCCTGTGGACAAGAAGTCACT	120
D	b142	atcaacttgcgaaggagtccaggaattaatlgttatthaatttgatttcacaagaacca	201
Oy	121	CCTACTTGTCGGCGAAGTCAGAGCATTTGATTAACTTACATTTGGCTTAGCGAGAACCA	180
D	b202	gggsaaatcctctaagacctgatattalcgycgcaatatgatltgatagatgggtcccatta	261
Oy	181	GATGAACCTATTAAACCCCTGATCTATGACCAATCCAGTTTAAGTCTGTGTGCCAAA	240
D	b262	agtttcagttgcagttgattctgcgcgaagtttaactcttcacacacagcgccgtgaatat	321
Oy	241	AGGTTCACTAGTGCACATAAGTCTGGSTGTGATATTATCTCTCACATCAGACACCTTGAGTCT	300
D	b322	gaagatatgygaacttattatgtctcagtltygatyagttccogtgygatgtcsgtlyga	381
Oy	301	GAATATTTTTGAGCCTATATTACTGCTCAAATATGCTAGTTCGCTGACAGTTCGGAGGG	360
D	b382	ggcccccaagcgcggaaaatcaaacggcgctgagatgctgcaccacactcttcacattccacca	441
Oy	361	GGGACCAAGCTGGAAATTAACGGGCTGATGCTGCACCAACTGATCAATCTTCCACCA	420
D	b442	tccagc 447	
Oy	421	TCCAAT 426	
RESULT	14		
ID	T99434 standard; cDNA: 447 BP.		
AC	T99434;		
DT	27-APR-1998 (first entry)		
DE	Anti-idiotypic antibody 3H1 light chain variable region cDNA.		
KW	Anti-idiotypic antibody 3H1; carcinoembryonic antigen; CEA;		
KX	tumour-specific antigen; tumour; colorectal cancer; lung cancer;		
OS	adenocarcinoma; therapy; SS.		
Mus musculus.			
FH Key	Location/Qualifiers		
FT	CD5		
FT	22..447		
FT	/ *tag= a		
PN	WO9738725-A1.		
PD	23-OCT-1997.		
PR	11-APR-1997; UO5953.		
PF	09-APR-1997; US-631085.		
PS	12-APR-1996; US-631085.		
(KENT) UNIV KENTUCKY.			
Chatterjee M. Chatterjee SK, Foon KA;			
WP1: 97-526218/48.			
DR	P-PDSB; W26727.		
PT	Use of anti-idiotypic antibody 3H1 - for delaying development of		
PT	carcinoembryonic antigen associated tumours		
PS	Disclosure: Page 38; 66pp; English.		
CC	This cDNA sequence includes a coding region for the light chain		
CC	variable region (VL) (see W26728) of murine monoclonal anti-idiotypic		
CC	antibody 3H1. A cDNA sequence (see T99435) for the VH region (see		
CC	W26729) is also provided. These clones can be utilised in the		
CC	recombinant production of 3H1 polypeptides. 3H1 induces a specific		
CC	immune response against a distinct and specific epitope of		
CC	carcinoembryonic antigen (CEA), a tumour-associated antigen. The		
CC	cDNA invention provides methods of delaying development of CEA-associated		
CC	tumours using 3H1, particularly in high-risk individuals. The		
CC	method can be used to delay the development of a variety of tumours,		
CC	including colorectal, gastric and pancreatic tumours, as well as		
CC	other adenocarcinomas such as those of the breast and lung, and		
CC	biliary cancer, and gynaecological cancers.		
SQ	Sequence 447 BP; 118 A; 101 C; 102 G; 126 T;		
Query Match	52.4%; Score 228; DB 38; Length 447;		
Best Local Similarity	76.8%; Pred. No. 7,81e-142;		
Matches 327; Conservative	0; Mismatches 99; Indels 0; Gaps 0;		
D	b22	atgcatcacacagcgcattccttgtatcctgttgcctgqtlltccaqqratcaatct 81	

QY	1	ATGGGGGGCCCTGCTCAGATCTTGGGTTCGTGTTGCTCTTGTTCCAGGTACCAAGATG	60
Db	82	gacatcaagatgaccagctccatcttccatgcatgcatcctctaggagagagttcag	144
QY	61	GACATCCAGATGACCCAGGTCTCCATCTCCATTCTGCTCTCTCGGACAAAGAGTCAGT	120
Db	142	atcacttgcgaaggcgagtcaggaatcaatgaagttatattaattggttccaaagaacca	204
QY	121	CTCACTTGTCCGGGGAAGCAGAGCATTGGATTAACATTACATTGGCTTCAGCAGGAACCA	180
Db	202	gggaatctccctagaccctcattatcgtgcgaatagattgatagatgggtcccatca	264
QY	181	GATGGAACTATTAAACGCTTATCTATACGCCACATCCAGTTAGCTTGTGGTGTCCAAA	240
Db	262	aggttcagttgcagttgatactgcgcaagtcttactctctccacacacagcagcctggaatat	324
QY	241	AGGTTCAATGGCAGTAGTCTGGGTCAGATTATTTCTCAACATCAGACAGCTTGAGTCT	300
Db	322	gaagatatgggaacttatttgtctccagtttgcagttgcagttcccgtagatgttcgttga	384
QY	301	GAAAGATTTTGTAGCCTATTACTGTCTCAATAATGCTAGTTCTCGGTACAGTTGGGAGGG	360
Db	382	ggcaccaagctcgggaatcaaacaggcggtcgatgctgcacccaactgctccatcttccacca	444
QY	361	GGGACCAAGCTGGAAATTAACGGGCGTGAATCTGCACCACTGTATCATCTTCCACACA	420
Db	442	tccagt 447	
QY	421	TTCAGT 426	

ID	RESULT	15	CDNA	447	BP.
AC	T34541	standard;	CDNA;	447	BP.
AC	T34541				
DT	11-OCT-1996	(first entry)			
DE	Monoclonal anti-idiotype antibody 3H1 VL CDNA.				
KM	Anti-idiotypic antibody; monoclonal antibody; CEA;				
KW	carcinoembryonic antigen; tumour-associated antigen; cancer;				
KW	vaccine; immunotherapy; ss.				
OS	Mus sp.				
PH	Key	Location/Qualifiers			
FT	cds	22..447			
FT		/*tag= a			
PN	W09620219-A2.				
PD	04-JUL-1996.				
PF	28-DEC-1995; U17105				
PF	28-DEC-1994; US-365484.				
PA	(KENT) UNIV KENTUCKY.				
PI	Chatterjee M, Chatterjee SK, Foon KA, Kohler H;				
DR	WPI, 96-321809/32.				
DR	P-PDSB; R99686.				
PT	Monoclonal anti-idiotype antibody 3H1 - elicits an immune response				
PT	to carcinoembryonic antigen				
PS	Example 2; Fig 1A; 102pp; English.				
CS	A CDNA clone (T34541) codes for the light chain variable region				
CC	(R99686) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 12003) .				
CC	It was obt'd. by PCR amplification (see also T34545-46) of CDNA				
CC	derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1				
CC	elicits a specific immune response to a unique epitope of				
CC	carcinoembryonic antigen (CEA) that is not present on other				
CC	members of the CEA family or on normal adult tissues. 3H1				
CC	can be used as a vaccine to elicit immune responses in patients				
CC	with advanced CEA-associated disease or, when labeled, to enhance				
CC	tumour detection in imaging.				
SC	Sequence 447 BP; 118 A; 101 C; 102 G; 126 T;				
Query Match	52.4%;	Score 228;	DB 22;	Length 447;	
Best Local Similarity	76.8%;	Pred. No. 7,81e-142;			
Matches 327;	Conservative 0;	Mismatches 99;	Indels 0;	Gaps 0;	
DB	22 atgcgtatcacagctcagcttccttggtatctctgttgcctcgtggttcacagtataatct 81				

```
QY 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCAGTACCAGATGT 60
Db 82 gacatcaagatgaccaggtctccatcttccatglatgcatctctagagagagatcaag 141
QY 61 GACATCCAGATGACCAAGTCCATCCCTTATCTGCTCTGCGACAAAGAGTCAGT 120
Db 142 atcacttgcaggcgagtcagacattaatgttatttaattgtgttcacaagaaccca 201
QY 121 CTCACTTGTGCGGCAAGTCAGACATTGGTATTAATTACATTGGCTTCAGCAGGAAACCA 180
Db 202 gggaaatctccaaagaccctatctatcgtgcnaatagattgatatagatgggtcccatca 261
QY 181 GATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 240
Db 262 aggttcagtgagcaatgcatctgggcaagttactctccaccatcagcagcctggaaatat 321
QY 241 AGGTTCAGTGGCAGTAGGCTGGGTGAGATTATCTCTCACCATCAGCAGGCTTGAGTCT 300
Db 322 gaagataatgggaacttattatgtctacagtttgatgagttccgltggatgttcggtgga 381
QY 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTCTCCGTACACGTTCCGAGGG 360
Db 382 ggcaccaagctgnaaatcaaacgggctgagtctgcaccaactgtctccatcttccacca 441
QY 361 GGGACCAAGCTGGAATTAACGGGCTGATGCTGCACCAACTGTATCCATCTCCACCA 420
Db 442 tccagct 447
QY 421 TCCAGT 426
```

Search completed: Sat Apr 17 14:55:13 1999
Job time : 222 secs.

THIS PAGE BLANK (USPTO)

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056
Fax: 3018699423

Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

FEATURES

source

1. .393
location/Qualifiers

mrna /organism="Homo sapiens"

BASE COUNT 88 a 113 c 96 g 94 t 2 others

ORIGIN

Query Match 40.2%; Score 175; DB 16; Length 393;

Best Local Similarity 72.7%; Pred. No. 0.00e+00;

Matches 285; Conservative 0; Mismatches 106; Indels 1; Gaps 1;

1 CCGGCTCAGCTCCGCGGCTCTCTACTCTGCTCGAGTGGCCAGATGTGACATCCA 60
9 CCTGCTCAGATCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 68

61 GATGACCCAGTCTCCATCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120

69 GATGACCCAGTCTCCATCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 128

121 CCGGCAAGTCT 180

129 TCGGCAAGTCT 188

181 CCTTACCT 240

189 TATTACCT 248

241 TGGCTCTGATCT 300

249 TGGCTCTGATCT 308

301 TGCACCT 360

309 TGTAGCT 367

361 AGGTGAGTCT 392

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

368 AGCTGGAATCT 399

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
location/Qualifiers
1. .413
/organism="Homo sapiens"
/note="Organ: testis; Vector: pBluescript SK-; Site:1;
/db_xref="taxon:9606"
/clone_lib="testis tumor"
/sex="male"
/dev_stage="adult"
/dev_stage="adult"

BASE COUNT 100 a 110 c 105 g 98 t

ORIGIN

Query Match 38.4%; Score 167; DB 24; Length 413;

Best Local Similarity 72.2%; Pred. No. 0.00e+00;

Matches 280; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

18 ATGAGGCTCCCGCTCAGCT 77

1 ATGGGGGCGCTGCTGATCT 60

78 GACATTCAGATGACCCAGTCT 137

61 GACATTCAGATGACCCAGTCT 120

138 ATCACTGCGGCGCTGCGGAGCATTAACACCATTTAATTGGTTCACAGAAACCA 197

121 CTCACCTTGTGGGAGCAATGAGATTTGATTTACTTACATTTGGCTTCAGAGAAACA 180

198 GGGAAAGCCCTTACGCTCTGATGTATGTATGATCCAGTTGCAAGGTGGGCTCTTCA 257

181 GATGACCTTTAATAGCCCTGATCTATAGCCACATCCAGTTAGTTGTGTTGCCAA 240

258 AGTTTCACTGCGGCTGATCTGAGAGATTTCACTCACTCACTCACTCACTCACTCACT 317

241 AGTTTCACTGCGGCTGATCTGAGAGATTTCACTCACTCACTCACTCACTCACTCACT 300

318 GAAATTTTCACTTCT 377

301 GAAATTTTGTAGCTTATCTGTTCAATATGCTTATGCTTCTGTTCCGTACAGG 359

378 AGGAGCAAGTGGAAATCAAGAGACT 405

360 GGGAGCAAGTGGAAATCAAGAGGCT 387

RESULT 3
LOCUS AA295786 382 bp mrna EST 18-APR-1997
DEFINITION EST100987 Pancreas tumor I Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:L01279), mRNA sequence.

Accession	Keywords	Source	Organism
AA295786	EST.	human.	homo sapiens
G1948121	EST.	human.	Eukaryote: mitochondrial eukaryotes; Metazoa: Chordata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
REFERENCE	AUTHORS		
	1 (bases 1 to 382)		
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., White,C.J., Lee,N.H., Kirness,E.F., Weinstein,K.G., Gocayne,J.D., Bilt,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wa,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hynes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Li,H., Li,I., Marmaros,S.M., Merrick,J.M., Moreno-Palmarques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bebnarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.F., Ferrie,A.C., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,D., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.		
	Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence		
	Nature 377 (6547 Suppl.), 3-174 (1995)		
JOURNAL MEDLINE			
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: akkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/ngi/ngi.html) Seq primer: M13 Reverse.		
FEATURES	source	Location/Qualifiers	
		1..382	
		/organism="Homo sapiens"	
		/note="Organ: Pancreas; Vector: pBluescript SK-; Site_1: EcoRI, Site_2: XhoI"	
		/db_xref="ATCC (inhost):191223"	
		/db_xref="taxon:9606"	
		/clone_id="Pancreas tumor I"	
		/dev_stage="adult"	
		<1..>382	
BASE COUNT	83 a	102 c	96 g 94 t 7 others
ORIGIN	mRNA		
	Query Match 37.7%; Score 164; DB 24; Length 382;		
	Best Local Similarity 73.3%; Pred. No. 0.00e+00;		
	Matches 261; Conservative 0; Mismatches 94; Indels 1; Gaps 1;		
	28 ATGAGGTCCTCCGCTCAGCTCTGGGGCTCTGCTACTGTGCTCGAGTGCCAGATGT 87		
	1 ATGGGGGCCCTCGTCAGATCTTGGGGTTCTTGTTGCTCTTGTTCCAGGTACAGATGT 60		
	88 GACATCCGATGACCCAGTCATCTCCCTCCCTGCTCATCTGTGGGNGACAGATCACC 147		
	61 GACATCCGATGACCCAGTCATCTCCCTCTTATCTGCTCTCGGGACAAAGATCAGT 120		
	148 ATCATTCGCGGGCAGGTCAAGGACATTAGCACTTTTAAATTGGTATCCACGAGACCA 207		
	121 CTCATCTGTGGGCAAGTCAGACATGTGATTAACTTACATTGCGCTTCACGAGAACCA 180		
	208 GGTAAAGCCCTAAAGCTCTGATCTATGACACCTCCACAGTTTGCAAGTGGGGTCCATCA 267		

Oy	161	GATGCACTATTAAACGCCCTGATCTACAGCCACATCCAGTTTAGGTTCTGTGTCGCCAAA	240
Db	268	AGGTTTCAGTGGCAGTGGATCTGGAGCAGATTCAGTCTCAGCATCAGCAGTCTGCAANCT	327
Oy	241	AGGTTTCAGTGGCAGTGGATCTGGAGCAGATTCAGTCTCAGCATCAGCAGTCTGCAANCT	300
Db	328	GAGGTTTTCAGTGGATCTGGAGCAGATTCAGTCTCAGCATCAGTCTGCAANCT	362
Oy	301	GAGGTTTTCAGTGGATCTGGAGCAGATTCAGTCTCAGCATCAGTCTGCAANCT	356
RESULT	4	AA335086	345 bp mRNA EST 21-APR-1997
LOCUS		EST39457	Esophagus tumor Homo sapiens cDNA 5' end similar to
DEFINITION		immunoglobulin kappa light chain, V region, mRNA sequence.	
ACCESSION		AA335086	
NTD		g1987349	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;	
AUTHORS		Homo.	
		1 (bases 1 to 345)	
		Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,	
		Bult,C.J., Lee,N.H., Kirkness,E.F., Weissbrock,K.G., Gocayne,J.D.,	
		White,O., Sutton,G., Blake,J.A., Brannon,R.C., Maniatis,C.,	
		Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,	
		Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghegan,N.S.,	
		Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,	
		Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merick,J.M.,	
		Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,	
		Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,	
		Smell,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Wiley,	
		Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,	
		Dimke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A.,	
		He,W.W., Hu,J.S., Kirsch,J.M., Gruber,J., Hudson,P., Kim,A.K.,	
		Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,	
		Ramond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,	
		Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,	
		Fraser,C.M. and Venter,J.C.	
TITLE		Initial assessment of human gene diversity and expression patterns	
JOURNAL		based upon 83 million nucleotides of cDNA sequence	
MEELINE		Nature 377 (6547 Suppl), 3-174 (1995)	
COMMENT		96026280	
		Other ESTs: EST39456 TNC167177	
		Contact: Kerlavage, AR	
		Bioinformatics	
		The Institute for Genomic Research	
		9712 Medical Center Drive, Rockville, MD 20850 USA	
		Tel: 3018699056	
		Fax: 3018699423	
		Email: arkerlavage@tigr.org	
		For clone availability, additional sequence and expression	
		information related to this EST, please check the TIGR Human Gene	
		Index (http://www.tigr.org/tgdb/hgi.html)	
		Seq primer: M13 Reverse.	
FEATURES		Location/Qualifiers	
SOURCE		1..345	
		/organism="Homo sapiens"	
		/note="Organ: esophagus; Vector: pBluescript SK-; Site_1:	
		EcotRI, Site_2: XhoI"	
		/db_xref="ATCC (inhost):136612"	
		/db_xref="taxon:9606"	
		/clone_lib="Esophagus tumor"	
		/dev_stage="adult"	
		<1..>345	
BASE COUNT		81 a 100 c 79 g 85 t	
ORIGIN			
Query Match		37.5%;	Score 163; DB 25; Length 345;
Best Local Similarity		74.8%;	Pred. No. 0.00e+00;
Matches		246; Conservative	0; Mismatches 83; Indels 0; Gaps 0;

Db 6 ATGAGGTCCTCCGCTCAGCTCCTGGGCTCCTGCTACTCTGGCTCCAGTCCAGATGCT 65
 1 ATGGGGGCCCCCTGGCTCAGATTCCTGGGCTTGGTCTGGTCCAGGATCCAGATG 60
 Oy 1 ATGGGGGCCCCCTGGCTCAGATTCCTGGGCTTGGTCTGGTCCAGGATCCAGATG 60
 Db 66 GACATCCAGATGACCCAGTCTCCATCCCTGCTGTCGATCTGTAGAGAGATGAC 125
 1 GACATCCAGATGACCCAGTCTCCATCCCTGCTGTCGATCTGTAGAGAGATGAC 120
 Oy 61 GACATCCAGATGACCCAGTCTCCATCCCTGCTGTCGATCTGTAGAGAGATGAC 120
 Db 126 ATCACTGCGCGGAGTCAAGCATTAGACACCATTTAAATGGTATCAACAAAACCT 185
 121 CTCACCTGTCGCGGAGTCAAGCATTAGATTAATTAATTAATTAATTAATTAATTA 180
 Oy 121 CTCACCTGTCGCGGAGTCAAGCATTAGATTAATTAATTAATTAATTAATTAATTA 180
 Db 186 GGGAAAGCCCTAGCTCCTGATCTATGTCGATCCAGATTTGGCAACGGGGTCCCATCA 245
 181 GAGGAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
 Oy 181 GAGGAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
 Db 246 AGTTTCAGTGGGCTGCTGGAGATTTACATTCATCCATCAGATCAGATCCATCC 305
 241 AGTTTCAGTGGGCTGCTGGAGATTTACATTCATCCATCAGATCAGATCCATCC 300
 Oy 241 AGTTTCAGTGGGCTGCTGGAGATTTACATTCATCCATCAGATCAGATCCATCC 300
 Db 306 GACGCTTTGCACTTATTTACTGTACACA 334
 301 GAGATTTTGTAGCTATTTACTGTACACA 329
 Oy 301 GAGATTTTGTAGCTATTTACTGTACACA 329

RESULT 5
 LOCUS AA301261 352 bp mRNA EST 18-APR-1997
 DEFINITION EST14181 Testis tumor Homo sapiens cDNA 5' end similar to
 immunoglobulin kappa light chain, V region, mRNA sequence.
 AA301261
 ACCESSION g1953592
 NID EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homnidae;
 Homo.
 1 (bases 1 to 352)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gockyne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.,
 Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegriano,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melisner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M., and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 JOURNAL MEDLINE
 COMMENT Other-ESTs: TH167177
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: atkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/ngi/ngi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers

source 1..352
 /organism="Homo sapiens"
 /note="Organ: testis; Vector: pBluescript SK-; site_1:
 EcoRI; site_2: XhoI"
 /db_xref="ATCC (inhost):191747"
 /db_xref="taxon:9606"
 /clone_lib="Testis tumor"
 /sex="male"
 /dev_stage="adult"
 <1..>352
 BASE COUNT 84 a 94 c 83 g 88 t 3 others
 ORIGIN

Query Match 37.5%; Score 163; DB 24; Length 352;
 Best Local Similarity 75.4%; Pred. No. 0.00e+00;
 Matches 248; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

Db 1 TGAGGGTCCCGCTGAGCTCCTGGGCTCCTGCTACTCTGGCTCCAGTCCAGATG 60
 Oy 2 TGAGGGGCCCCCTGGCTCAGATTCCTGGGCTTGGTCTGGTCCAGGATCCAGATG 61
 Db 61 ACATCCAGATGACCCAGTCTCCATCCCTGCTGTCGATCTGTAGAGAGATGACCA 120
 Oy 62 ACATCCAGATGACCCAGTCTCCATCCCTGCTGTCGATCTGTAGAGAGATGAC 121
 Db 121 TCACCTGCGGCGGAGTCAAGCATTAGACACCATTTAAATGGTATCAACAAAAC 180
 Oy 122 TCACCTGCGGCGGAGTCAAGCATTAGATTAATTAATTAATTAATTAATTAATTA 181
 Db 181 GGAAGGCCCTAGCTCCTGATCTATGTCGATCCAGATTTGGCAACGGGGTCCCATCA 240
 Oy 182 ATGGAACCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 241
 Db 241 GGTTCAGTGGGCTGCTGGAGATTTACATTCATCCATCAGATCAGATCCAAACT 300
 Oy 242 GGTTCAGTGGGCTGCTGGAGATTTACATTCATCCATCAGATCAGATCCAAACT 300
 Db 301 GAAGCTTTTGCATTTACTGTACACA 329
 Oy 301 GAAGATTTTGTAGCTATTTACTGTACACA 329

RESULT 6
 LOCUS R67559 516 bp mRNA EST 30-MAY-1995
 DEFINITION y142h11.r1 Homo sapiens cDNA clone 141957 5' similar to
 gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);.
 ACCESSION R67559
 NID 9840197
 KEYWORDS EST.
 SOURCE human clone=141957 library=Soares placenta Nb2HP vector=pf773D
 (Pharmacia) with a modified polylinker host=PH10B (ampicillin
 resistant) primer=M13RPI Rsitel=Not I Rsitel2=Eco RI Female placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 AACTGGAAGAATTCGCGGCCGAGATTTTCTTTTCTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified p773
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bernaldo.

ORGANISM Homo sapiens
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Carnivora; Homnidae; Homo.
 1 (bases 1 to 516)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Merritt,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P., and
 Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE JOURNAL
 COMMENT

SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 303)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bull,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednariik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other-ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source
1..303
/organism="Homo sapiens"
/note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):191887"
/db_xref="taxon:9606"
/clone_lib="Testis tumor"
/sex="male"
/dev_stage="adult"
<1..>303
BASE COUNT 70 a 83 c 75 g 70 t 5 others
ORIGIN
Query Match 35.4%; Score 154; DB 24; Length 303;
Best Local Similarity 75.4%; Pred. No. 2,92e-284; Indels 0; Gaps 0;
Matches 221; Conservative 0; Mismatches 72;

Db 247 AGCTTCAGTGGCAGATGTCGGGCGAGATTTCATCTCACCGTCAGCT 299
Qy 241 AGGTCAGTGGCAGATGTCGGGCGAGATTTCATCTCACCGTCAGCT 293

RESULT 9
LOCUS AA361497 357 bp mRNA EST 21-APR-1997
DEFINITION EST1040 T-cell lymphoma Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence.
ACCESSION AA361497
NID 92014052
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 357)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bull,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednariik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other-ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source
1..357
/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):165882"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
<1..>357
BASE COUNT 88 a 96 c 84 g 87 t 2 others
ORIGIN
Query Match 35.2%; Score 153; DB 25; Length 357;
Best Local Similarity 74.3%; Pred. No. 6.04e-282; Indels 2; Gaps 2;
Matches 246; Conservative 0; Mismatches 83;

Db 6 ATGAGGTCGCCGCTCAGCTCTGCGGCTCCTGCTACTGCTCGAGTGCACATG 65
Qy 1 ATGGGGGCCCTCCTCAGATTCCTGGGTTCTGTGCTCTTCCAGTACCATGT 60

Db 187 GGGAAAGCCCCCTAACTCTGATCTATGCTCATCAGTTGCAAGAGTGGGTCCCATCA 246
Qy 181 GATGAACTATTAAGCGCTGATCTACGCCACATCCAGTTTAAAGTTCTGGTGTCCCAA 240

Db 66 GACATCCAGATGACCAGTCTCCTCTGTCATCTGTAGAGAGACAGATCACC 125

Qy	61	GACATCCCGAGTACCGCAGTCCCTCCCTTATCTCCCTCTCGGACAAAGAGTCAgT	120
Db	126	ATCACTTGGCGGGGCAAGNMGASATTAACAACATATTAAATGGTATCAACAGAAACCA	185
Qy	121	CTCACTTGTGGGGCAAGTCAGACGACATTGGTATTTAACCTTACATTGGCTTACCGAGAACCA	180
Db	186	GGGAAAGCCCTAAGCTTCCTGATCTACGGTCATCCAGTCTGCMAAGTGGGGGTCCCATC	245
Qy	181	GATGGAACTATTAAACGGCTGATCTACGCCACATCCAGTTAGGTCTGGCTGCCCAA-	239
Db	246	AAGGTCTAGTGGCAGTGGATCTGGACAGATTTCATCTCANCATCAGGGGTGCAAC	305
Qy	240	AAGGTCTAGTGGCAGTGGATCTGGGTCAAGATTAT-CTCTCACATAGACAGCCTTGAGT	298
Db	306	CTGAAGATTTCACAATTACTACTCTCAACA	336
Qy	299	CTGAAGATTTTGTAGCCATTACTGTCTACA	329

RESULT 10 AA300788 303 bp mRNA EST / 18-APR-1997
 DESCRIPTION ES131648 Testis tumor, Homo sapiens CDNA 5' end similar to
 immunoglobulin kappa light chain, V region, mRNA sequence.
 ACCESSION AA300788
 NID g1953120
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 303)

AUTHORS
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulder, R.A.,
 Butt, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Maniwal, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.W., Fitzhugh, W.M., Fitchman, J.L., Geoghagen, N.S.,
 Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Seudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utteback, T.R., Weidman, J.F., Li, Y.,
 Behnathik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dinke, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kosak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J.C., Xu, C., Yu, G. L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
LE
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (5547 Suppl.), 3-174 (1995)

FEATURES
source

```

/organism="Homo sapiens"
/ncbi:organ:taxid:9606
/ecori:site:2:"XhoI"
/db_xref="ATCC (inhost):192224"
/db_xref="taxon:9606"

```

	/clone_lib="testis tumor"			
	/sex="male"			
	/dev_stage="adult"			
mRNA	<1. .>303			
BASE COUNT	69 a	88 c	72 g	72 t
ORIGIN				2 others

Query Match	34.7%;	Score 151;	DB 24;	Length 303;
Best Local Similarity	75.4%;	Pred. No. 2.57e-277;		
Matches 221;	Conservative	0;	Mismatches 72;	Indels 0;
				Gaps 0

Db 8 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT 67

2Y 1 ATGGGGGCCCTGCTCAGATTCTGGGTCTTGCTCTTGTTCCAGGTACCAGATGT 600

Db 68 NACATCCAGATGACCCAGTCTCCATCTCCCTGTGTCATCTGTAGGAGACAGAGTCAAC 12

01 GACATCCAGATGATCCAGTCTCCATCCCTTATCTGCTCTCTGGACAAAGAGTCAGT 12

[illegible]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
--	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

[illegible]

248 **АССИМИЛАНТИЗМ** 300

241 AGGTTAGTGGCAGTAGGTTCTGGGTCAAGATTATTCTCTCAACCATCAGCAGCCT 293

LOCUS	AA300491	282 bp	mRNA	EST	18-APR-1997
LOCUS	AA300491	282 bp	mRNA	EST	18-APR-1997

immunoglobulin kappa light chain, V region, mRNA sequence.

NID
REVLOPNC
FCM
g1952905

SOURCE	human.
ORGANISM	Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homini

REFERENCE 1 (bases 1 to 282)

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P.S.Jr.

Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligri
Phillips, C.A., Ryder, S.E., Scott, J.T., Sauder, D.M., Shrivley, F.

Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.

Chen, D., Feng, D.-F., Feilcke, A., Fischner, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Fraser, C.M. and Venter, J.C.

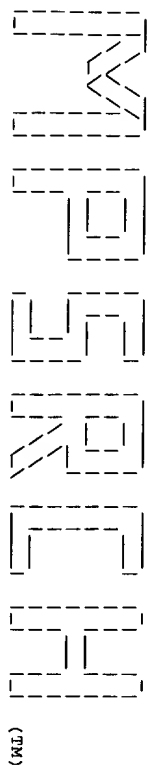
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl) 3-174 (1995)

MEDLINE 96026280
COMMENT Other ESTs: THC167177

CONTACT: KeriLavage, AR
Bioinformatics

9712 Medical Center Drive, Rockville, MD 20850 USA

Fax: 3018699423



Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 15 18:01:37 1999; MasPar time 7.49 Seconds

Car output not generated. 330.677 Million cell updates/sec

Title: >US-08-836-455-4

Description: (1-153) from US08836455.pep

Perfect Score: 1109

Sequence: 1 MECSWVFLFLSLITGVHSQ.....TVSAAKTPPPYPLVPGSL 153

Scoring table:

PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

a-genesec32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 30.945; Variance 171.704; scale 0.180

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1109	100.0	153	25	W27120	Murine monoclonal ant	1.22e-73
2	850	76.6	465	13	R66758	Anti-tobacco mosaic v	6.81e-54
3	820	73.9	159	1	P93079	Heavy chain of monocl	1.29e-51
4	798	72.0	468	3	R13061	Monoclonal antibody O	6.01e-50
5	774	69.8	469	8	R40384	Monoclonal antibody M	3.95e-48
6	768	69.3	463	22	W14940	3F4 (Chimeric) human	1.13e-47
7	768	69.3	463	22	W14939	3F4 (Chimeric) human	1.13e-47
8	768	69.3	464	22	W14938	Murine anti-porcine v	1.13e-47
9	768	69.3	464	22	W14941	3F4 Human IgG4 expres	1.13e-47
10	755	68.1	140	29	W41070	Mouse 2H7 antibody he	1.08e-46
11	755	68.1	140	29	W47513	Mouse 2H7 antibody he	1.08e-46
12	755	68.1	140	29	W47520	Mouse 2H7 antibody he	1.08e-46
13	752	67.8	140	23	W16343	2H7 heavy chain varia	1.83e-46
14	752	67.8	140	1	P94780	2 H7 VH gene.	1.83e-46
15	752	67.8	140	22	W10242	Heavy chain variable	1.83e-46
16	752	67.8	140	23	W10588	2H7 antibody heavy ch	1.83e-46
17	749	67.5	140	2	P70627	Sequence encoded by t	3.08e-46
18	745	67.2	590	28	W31751	H chain subunit of Fa	6.19e-46

19	742	66.9	464	13	R76088	MAB 55.1 heavy chain.	1.04e-45
20	741	66.8	235	7	R41682	Cimeric antibody comp	1.24e-45
21	736	66.4	235	7	R41715	Murine 128.1 VH/human	2.96e-45
22	736	66.4	235	7	R41707	Murine 128.1 VH/human	2.96e-45
23	735	66.3	136	1	P93151	Protein encoded by V	3.53e-45
24	735	66.3	136	10	R59510	Sequence of the heavy	3.53e-45
25	730	65.8	141	5	R09427	ME4 Heavy Chain V Reg	8.42e-45
26	730	65.8	141	20	W06216	MAB ME4 heavy chain v	8.42e-45
27	728	65.6	118	25	W27122	Murine antibody heavy	1.19e-44
28	720	64.9	140	20	W06213	MAB Co-1 heavy chain	4.80e-44
29	719	64.8	144	2	R08346	Heavy chain variable	5.71e-44
30	716	64.6	233	7	R41710	Murine 128.1 VH/human	9.62e-44
31	713	64.3	139	28	W36167	Heavy chain variable	1.62e-43
32	711	64.1	137	12	R62445	81C6 heavy chain vari	2.26e-43
33	711	64.1	139	25	W29750	Anti-HMG MAB CTMO1 h	2.29e-43
34	710	64.0	138	27	W34515	Variable heavy chain	2.73e-43
35	710	64.0	140	5	R09425	Co-1 Heavy Chain V Re	2.73e-43
36	704	63.5	139	7	R33950	CTMO1 VH.	7.74e-43
37	704	63.5	249	15	R77609	Chimeric heavy chain	7.74e-43
38	703	63.4	163	3	R15200	R6-5-D6 anti-ICAM-1 h	9.21e-43
39	703	63.4	163	3	R15060	Murine anti-ICAM mono	9.21e-43
40	701	63.2	137	20	W03724	Anti-human gp39 MAb 3	1.30e-42
41	699	63.0	140	10	R55554	DREG-200 Ab heavy cha	1.85e-42
42	697	62.8	137	2	R12238	Mouse MAb 4D12 H chal	2.61e-42
43	697	62.8	137	2	R12360	Heavy chain variable	2.61e-42
44	686	62.8	140	11	R55215	Murine variable regio	3.11e-42
45	695	62.7	136	20	W06446	HuM3 VH region BR-R	3.70e-42

ALIGNMENTS

RESULT	1	W27120 standard; Protein; 153 AA.
AC	W27120;	
DT	04-JAN-1998	(first entry)
DE	Murine monoclonal anti-idiotypic antibody 11D10 VH region.	
KW	Monoclonal antibody 11D10; anti-idiotypic antibody; mAb; human milk fat globule; HMGF; tumour; breast cancer; vaccine.	
OS	Mus musculus.	
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= sig_peptide
FT	Protein	20..153
FT		/label= Mat_protein
FT		20..49
FT	Region	/label= FRI
FT		/note= "framework region 1"
FT		50..54
FT		/label= CDR1
FT		/note= "complementarily determining region 1"
FT	Region	/label= FR2
FT		55..68
FT		/label= FR2
FT	Region	/note= "framework region 2"
FT		69..85
FT		/label= CDR2
FT		/note= "complementarily determining region 2"
FT	Region	86..117
FT		/label= FR3
FT		/note= "framework region 3"
FT		118..126
FT		/label= CDR3
FT		/note= "complementarily determining region 3"
FT	Region	127..137
FT		/label= FRI
FT		/note= "framework region 4"
FT	Region	138..153
FT		/label= Constant
FN	W09122699-A2.	
PD	26-JUN-1997.	
PR	19-DEC-1996; U20757.	
PR	13-DEC-1996; US-575762.	
PR	20-DEC-1995; US-575762.	
PR	26-JAN-1996; US-591965.	

PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR MPI: 97-212855/19.
 DR N-PSDB: T62938.
 PT Antibodies binding to porcine but not human cell interaction
 CC proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 62-64; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 464 AA:

Query Match 69.3%; Score 768; DB 22; Length 464;
 Best Local Similarity 72.1%; Pred. No. 1,13e-47;
 Matches 106; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

DB 4 SWFLFLSTTGVHSAAYLQSGAEIVRGASVKNKSCASGTLTISYNNHMKQTPGG 63
 QY 4 SWFLFLSTTGVHSAAYLQSGAEIVRGASVKNKSCASGTLTISYNNHMKQTPGG 63

DB 64 LEWIGALPGNGDCTYKFKYKATLVDKSSSTAYMQISLSEDSAVYFCARGNMEGA 123
 QY 64 LEWIGALPGNGDCTYKFKYKATLVDKSSSTAYMQISLSEDSAVYFCARGNMEGA 123

DB 124 fdwaggttlvtssasckgspvflap 150
 QY 124 fdwaggttlvtssasckgspvflap 150

DB 124 LDYWGQGTSTVTSAAKTPPPYPLVP 150
 QY 124 LDYWGQGTSTVTSAAKTPPPYPLVP 150

RESULT 10
 ID W41070 standard; Protein; 140 AA.
 AC W41070;
 DT 01-JUN-1998 (first entry)
 DE Mouse 2H7 antibody heavy chain variable region.
 KM Mouse; murine; heavy chain; variable region;
 KW immunoglobulin fragment production; Ig fragment production;
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= sig_peptide
 FT Peptide 20..140
 FT Peptide /label= mat_peptide

PN US5693493-A.
 PD 02-DEC-1997.
 PF 25-MAY-1995; 450731.
 PR 29-MAR-1990; US-501092.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 25-MAY-1995; US-450731.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL;
 DR MPI: 98-031749/03.
 DR N-PSDB: V03926.
 PT Production of chimeric antibody fragments - by culturing E. coli
 PS transformed with dicistronic expression cassette
 CC Example IV; Fig 21; 98pp; English.
 CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the

CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC against human B-cell surface antigen. The invention provides a
 CC novel approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 SQ Sequence 140 AA:

Query Match 68.1%; Score 755; DB 29; Length 140;
 Best Local Similarity 79.3%; Pred. No. 1.08e-46;
 Matches 111; Conservative 11; Mismatches 14; Indels 4; Gaps 2;

DB 1 mgfsrflflsvltgvsqaylqsgaeivrgasvknkscasgytfsymhmkqtp 60
 QY 1 MGSWFLFLSTTGVHSAAYLQSGAEIVRGASVKNKSCASGTLTISYNNHMKQTP 60

DB 61 rgglewigaalpbgndctyknqkfkqkattlvdkssstaymqislsedsavycarvvy 120
 QY 61 rgglewigaalpbgndctyknqkfkqkattlvdkssstaymqislsedsavycarvvy 120

DB 61 GQGLEWIGNIFPENGDTYYNOKFKGRASLTADTSSSTAYMQISLSEDSAVYFCARG-N 119
 QY 61 GQGLEWIGNIFPENGDTYYNOKFKGRASLTADTSSSTAYMQISLSEDSAVYFCARG-N 119

DB 121 ynsywyfdwgtgtlvtvs 140
 QY 121 ynsywyfdwgtgtlvtvs 140

DB 120 WEGA---LDYWGQGTSTVTS 136
 QY 120 WEGA---LDYWGQGTSTVTS 136

RESULT 11
 ID W47513 standard; Protein; 140 AA.
 AC W47513;
 DT 05-JUN-1998 (first entry)
 DE Mouse 2H7 antibody heavy chain variable region.
 KM Mouse; murine; heavy chain; variable region;
 KW immunoglobulin fragment production; Ig fragment production;
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= sig_peptide
 FT Peptide 20..140
 FT Peptide /label= mat_peptide

PN US5698435-A.
 PD 16-DEC-1997.
 PF 06-JUN-1995; 467140.
 PR 29-MAR-1990; US-501092.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 06-JUN-1995; US-467140.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL;
 DR MPI: 98-051492/05.
 DR N-PSDB: V18557.
 PT DNA encoding secretable immunoglobulin fragments - comprising at
 PS least the variable regions of light or heavy chains
 CC Example IV; Fig 21; 98pp; English.
 CC The present sequence was used in the development of a novel method


```

FT      region                               118..130
FT      /label= CDR3
FT      /note= "Complementarity determining region 3"
FT      region                               131..140
FT      /label= FR4
FT      /note= "framework region 4"
PN      US5618920-A.
PD      08-APR-1997.
PF      01-NOV-1985: 793980.
PF      01-NOV-1985: US-793980.
PR      27-OCT-1986: WO-002269.
PR      24-JUL-1987: US-077528.
PR      11-JAN-1988: US-142039.
PR      29-MAR-1990: US-501092.
PR      17-APR-1992: US-870404.
PR      29-APR-1994: US-235223.
PA      (XOMA ) XOMA CORP.
PI      Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI      Wall R, Wilcox GL;
PI      MPI: 97-225473/20.
DE      N-PSDB: T70868.
DE      Secreted immunoglobulin heavy and light chain fragments - capable
FT      of assembling into chimeric antibodies, useful for e.g. passive
FT      immunisation, diagnosis, etc
FT      Example 4; Fig 21: 96pp; English.
CC      A polypeptide (M16343) comprises the heavy chain variable region of
CC      mouse monoclonal antibody 2H7, which recognises human B-cell surface
CC      antigen Bp35. It is encoded by a cDNA clone (T70868) obt. from a
CC      2H7 cDNA library by PCR amplification. The 2H7 light chain variable
CC      sequence (M16344) is also provided. A novel human-mouse chimeric
CC      antibody with specificity for the human B-cell antigen has been
CC      constructed.
SQ      Sequence 140 AA:

```

Query Match	67.8%	Score 752;	DB 23;	Length 140;
Best Local Similarity	79.3%;	Pred. No. 1.83e-46;		
Matches 111;	Conservative 11;	Mismatches 14;	Indels 4;	Gaps 2;

Db	1	mgfsrflflsvltqvnsgaylqgsqgaelyrpsavkmsckasqyftfsymhwkqtp	60
	1		60
Qy	1	MECSWVFLFLSITTTGVHSAQVLIQSSGHELVRSASAKMSCKASGTYLTISNMHWKQTP	60
	61		60
	61	rgqlwlgalygpnqdsynqkfykattlvdkssstaysmqllstedsavfcarvy	120
	61		120
	61	GQGLEWIGNIPRPGNGDFTYNNKFKGKASLFDADTSSSTFAYMQISSLTSEDSAVFYCARNG-N	119
	121	ysnsywyfdvvgvtcttvtvs	140
			140
	120	MEGA--LDYWGQGTSTVTVS	136

RESULT	14
ID	P94780 standard; protein; 140 AA.
AC	P94780;
DT	06-JUL-1990 (first entry)
DE	2 H7 VH gene.
KW	Antibodies; passive immunisation; pH3-12a; ss.
OS	Synthetic.
Key	
FH	Location/Qualifiers
FT	1..19
FT	/label=Leader peptide.
FT	20..49
FT	/label=FR1.
FT	50..54
FT	/label=CDR1
FT	55..68
FT	/label=FR2
FT	69..85
FT	/label=CDR2.
FT	86..117
FT	/label=FR3.
FT	118..130
FT	/label=CDR3.
FT	domain

FT	domain	131..140
FT	/label=FR4.	
FT	domain	108..123
FT	/label=jK2	
PN	WO8900999-A.	
PD	9-FEB-1989.	
PF	25-JUL-1988:	02514
PR	24-JUL-1987:	US-077528.
PA	(INTE-) Int Genetic Eng. Inc.	
PI	Robinson RR, Lin AY, Horvitz AH, Wall R, Better M;	
PI	WPI: 89-061144/08.	
DR	N-PSDB: G91146.	
PT	Polyunucleotide(s) encoding Immunoglobulin molecules -	
PT	used for efficient prodn. of chimeric human or non-human or	
PT	class switched antibodies.	
PS	Disclosure: 7pp; English.	
CC	Sequence carries the variable region of the chimeric immunoglobulin	
CC	sequence. The antibodies are useful in passive immunisation avoiding	
CC	negative immune reactions. They are also useful in assaying and in vitro	
Q	imaging.	
Q	Sequence	140 AA;

Query Match	67.8%	Score 752;	DB 1;	Length 140;
Best Local Similarity	79.3%	Pred. No. 1,83e-46;		
Matches 111;	Conservative 11;	Mismatches 14;	Indels 4;	Gaps 2;
Db 1 mgfsrffllsvtgyhsagylqgsaaelvrrpagsakmsckasgyrftsynmhvkrqtp 60	: : : : : : : : : : : : : : : : : : : : : : : : :			
Qy 1 MECSWFLFLILSTTGYHSQARYLQSSAEELVRSASAKMSCKASGILTISYNMHVKQTP 60	: : : : : : : : : : : : : : : : : : : : : : : : :			
Db 61 rqlgiewigaaypngdcsynqkfkqkactllvdkssstaysmqslsleedsaayfcarvvy 120	: : : : : : : : : : : : : : : : : : : : : : : : :			
Qy 61 GQGLEMIIGNIRPGNGDRIYNNKFRGKASLADIRSSRAYNQISLSTSEDAVYFCARG-N 119	: : : : : : : : : : : : : : : : : : : : : : : : :			
Db 121 ysnasywyfdvwtgvtlvts 140	: : : : : : : : : : : : : : : : : : : : : : : : :			
Qy 120 WEGA---LDYWGQCTSYTVS 136	: : : : : : : : : : : : : : : : : : : : : : : : :			
RESULT 15				
ID W10242 standard; Protein; 140 AA.				
AC W10242;				
DT 06-AUG-1997 (first entry)				
DE Heavy chain variable sequence of 2H7.				
KW Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;				
KW protein production; human; constant region; passive immunisation; toxin;				
KW serum sickness; anaphylaxis; sweetener; thauminin; cytoplasm; periplasm;				
KW antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;				
KW myeloma cell.				
OS Mus musculus.				
FT key	Location/Qualifiers			
FT peptide	1..19			
FT region	/note="leader peptide"			
FT region	20..49			
FT region	/note="framework region 1"			
FT region	50..54			
FT region	/note="complementarity determining region 1"			
FT region	55..68			
FT region	/note="framework region 2"			
FT region	69..85			
FT region	/note="complementarity determining region 2"			
FT region	86..117			
FT region	/note="framework region 3"			
FT region	118..130			
FT region	/note="complementarity determining region 3"			
FT region	131..140			
FT region	/note="framework region 4"			
US5576195-A.				
PD 19-NOV-1996.				
PF 01-NOV-1985; 793980.				
PF 01-NOV-1985; US-793980.				
PR 27-OCT-1986; WO-002269.				
PR 24-JUL-1987; US-027528				


```

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6.
RX MEDLINE; 81234548.
RA BOWEN A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTI-BODIES).
CC EMBL; J00529; G195115;
DR PIR; A02034; MMS18.
DR HSSP; P01810; 1JHL.
DE IMMUNOGLOBULIN V REGION; SIGNAL.
ID SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; DEB2C7DA CRC32;

Query Match
Best Local Similarity 59.1%; Score 655; DB 1; Length 139;
Matches 93; Conservative 21; Mismatches 18; Indels 2; Gaps 2;

Db 6 IMFLATATGVHSDVQLOOQSGPELVKPGASVLSKASGYTTSTYMMHWKQRPGRGLE 65
QY :||||:||||| :||||:||||:||||:||||:||||:||||:||||:||||:
6 VFELFLSTTGVHSDVQLOOQSGAEIVRSASVMSKASGYTLTSTYMMHWKQTPGCG 65
DB WIGRIDPNSGGTYKNEKFKSKATLTVDKPSSTAYMOLSTLSEDSAVYVCAR 125
QY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
66 WIGNIFPGNDITYNOKFKGKASLTADTSSSTAYMOISLSEDSAVYFCAR 123
DB 126 FYWGGTTLTVSS 139
QY :||||:||||:
124 LDYWGQGSTVTVSS 137

RESULT 3
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DE 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH58 A1/A4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 85099340.
RX YANCOPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL; M13787; G466291;
DR PIR; A02029; HVM5A1.
DR HSSP; P01772; 1FOR.
DE IMMUNOGLOBULIN V REGION; SIGNAL.
ID SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH58 A1/A4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

```

```

FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; A60F2B13 CRC32;

Query Match
Best Local Similarity 58.2%; Score 645; DB 1; Length 117;
Matches 87; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

Db 5 WIFLFLSTGAGVHCOVQLOOQSGPELVKPGALVKSCKASGYTFSTYDINMWKQRPQGL 64
QY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
5 VFELFLSTTGVHSDVQLOOQSGAEIVRSASVMSKASGYTLTSTYMMHWKQTPGCG 64
DB 65 EWIGWYPDGSGTYKNEKFKSKATLTADKSSSTAYMOLSTLSEDSAVYFCAR 117
QY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
65 WIGNIFPGNDITYNOKFKGKASLTADTSSSTAYMOISLSEDSAVYFCAR 117

RESULT 4
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (108A).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 81245215.
RX GIYOL D., ZAKUT R., EFFRON K., RECHAVI G., RAM D., COHEN J.B.;
RL NATURE 292:426-430(1981).
DR EMBL; J00488; G554028;
DR PIR; A02041; HVM58A.
DR HSSP; P01789; 1IGI.
DE IMMUNOGLOBULIN V REGION; SIGNAL.
ID SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (108A).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 941C002E CRC32;

Query Match
Best Local Similarity 57.3%; Score 636; DB 1; Length 117;
Matches 86; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

Db 4 SWIFLFLSGTGVHSEVQLOOQSGPELVKPGASVKSCKASGYTTSTYMMHWKQSHGKS 63
QY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
4 VFELFLSTTGVHSDVQLOOQSGAEIVRSASVMSKASGYTLTSTYMMHWKQTPGCG 63
DB 64 LEWIGIYIPNGSGTYNOKFKSKATLTVDNSSSTAYMELSTLSEDSAVYVCAR 117
QY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
64 WIGNIFPGNDITYNOKFKGKASLTADTSSSTAYMOISLSEDSAVYFCAR 117

RESULT 5
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (REL. 01, CREATED)
DE 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (543).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 81234548.
RX BOWEN A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).

```

```

CC -1- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL: J00539; G195119; -
DR PIR: A02038; G2MS43.
DR HSSP: P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON_TER 137 137
SO SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;

Query Match
St Local Similarity 57.3%; Score 635; DB 1; Length 137;
Matches 90; Conservative 23; Mismatches 18; Indels 2; Gaps 2;

DB 6 IMFLATATGVSHVQVLOOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
QY 6 VFELLSITGVSHQAVLOOQSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65

DB 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 124
QY 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 124

DB 125 DWGQGTTLTVSS 137
QY 125 DWGQGTTLTVSS 137

DB 125 DWGQGTTLTVSS 137
QY 125 DWGQGTTLTVSS 137

RESULT 6
ID HV03_MOUSE STANDARD; PRT; 117 AA.
AC P01747;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
-1- THIS GEMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC EMBL: J00536; G554035; -
CC DR PIR: A02031; HYMS3.
CC DR HSSP: P01810; 1JHL.
CC KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SO SEQUENCE 117 AA; 13016 MW; 0F12FC8B CRC32;

Query Match
St Local Similarity 57.2%; Score 634; DB 1; Length 117;
Matches 75; Conservative 23; Mismatches 18; Indels 2; Gaps 2;

```

```

Matches 84; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

DB 6 ILFLVATATGVSHVQVLOOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
QY 6 VFELLSITGVSHQAVLOOQSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65

DB 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 117
QY 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 117

RESULT 7
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (102).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
-1- THIS GEMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC DR PIR: A02032; HYMS02.
CC DR HSSP: P01810; 1JHL.
CC KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SO SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match
St Local Similarity 55.5%; Score 616; DB 1; Length 117;
Matches 84; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

DB 6 ILFLVATATGVSHVQVLOOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
QY 6 VFELLSITGVSHQAVLOOQSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65

DB 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 116
QY 66 WIGRIHPSDSGTYYNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 116

RESULT 8
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (36-65).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
-1- THIS GEMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC DR PIR: A02032; HYMS02.
CC DR HSSP: P01810; 1JHL.
CC KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SO SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match
St Local Similarity 55.5%; Score 616; DB 1; Length 117;
Matches 84; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

```



```

FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA: 12890 MW: C97683A2 CRC32:

Query Match 53.5%; Score 593; DB 1; Length 117;
Best Local Similarity 74.1%; Pred. No. 3,64e-110;
Matches 83; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

Db 6 IMFLATATGVSQVLOOQPGAEVLVPGASVKSCKASAGTFTSYMMHWKORPGRGLE 65
: ||| : ||||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 6 VFLLSLITTVSHQATVLOQSGAEVLVSGASVKSCKASAGTFTSYMMHWKOTPGGLE 65

Db 66 WIGNIDPNSGCTKYNEKFKSKATLTVDKPSSTAYMQLSLSLSEDSAYVYCTR 117
||||| : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 66 WIGNIFPENGDTYYNQKFKKASLTADTSSSTAYMQLSLSLSEDSAYVYFCAR 117

RESULT 12
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
OS MUS MUSCULUS (MOUSE).
OC EUKAROTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 85099340.
RA YANCORPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL: M13788; G464292; -.
PIR: A02035; MHMSB4.
DR HSSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 B4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA: 12834 MW: 85692FE5 CRC32:

Query Match 53.0%; Score 588; DB 1; Length 117;
Best Local Similarity 72.3%; Pred. No. 5,64e-109;
Matches 81; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

Db 6 IMFLATATGVSQVLOOQPGAEVLVPGASVKSCKASAGTFTSYMMHWKORPGRGLE 65
: ||| : ||||| |||:|||||:|||||:|||||:|||||:|||||:|||||
QY 6 VFLLSLITTVSHQATVLOQSGAEVLVSGASVKSCKASAGTFTSYMMHWKOTPGGLE 65

Db 66 WIGNIDPNSGCTKYNEKFKSKATLTVDKPSSTAYMQLSLSLSEDSAYVYCTR 117
||||| : |||:|||||:|||||:|||||:|||||:|||||:|||||
QY 66 WIGNIFPENGDTYYNQKFKKASLTADTSSSTAYMQLSLSLSEDSAYVYFCAR 117

RESULT 13
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKAROTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE.
RX MEDLINE: 83075344.

```

```

RA KERRY M.N., FURHMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RL HOOD L.E.;
RA BLOODMISTRY 21:5415-5424(1982).
CC -1- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
CC -1- THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MHMSAE.
DR HSSP: P01772; IJGV.
RW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON TER 117 117
SO SEQUENCE 117 AA; 12983 MW; 1F6CC304 CRC32.

Query Match 53.0%; Score 588; DB 1; Length 117;
Best Local Similarity 72.4%; Pred. No. 5,64e-109;
Matches 84; Conservative 14; Mismatches 15; Indels 3; Gaps 2;

Db 4 LQSGPELVKFGASVKMSKASGTFTFDYRWKVKQSHGSKSLEIGDINPNNGSTYNQK 63
OY 23 LQSGAEELVRSAGVSKMSKASGYTLTSYMMHWKQTPGGGLEIGNIFPGNGDYNNQK 82
OY 83 FKGRATLTVDKSSSTAYMQLNSLSEDSAYYCCARDW--YFDVWAGTIVYSS 117
FKGRATLTVDKSSSTAYMQLNSLSEDSAYYFCARG-NMEGALDYWGQSTVYSS 137

RESULT 14
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (BC1).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; RODENTIA.
RN [1]
RA SEQUENCE FROM N.A.
RX KNPMP M.R., LIU C.-P., NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,
RA BLATTNER F.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).
DR EMBL; J00494; G195011; -.
DR PIR: A02042; HVMSBL.
DR HSSP: P01789; IJEL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT CHAIN 1 19
FT SIGNAL 20 136 IG HEAVY CHAIN V REGION (BC1).
FT NON TER 136 136
SO SEQUENCE 136 AA; 15078 MW; E04F1C7F CRC32.

Query Match 52.8%; Score 585; DB 1; Length 136;
Best Local Similarity 61.4%; Pred. No. 2,92e-108;
Matches 81; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Db 6 IIFELVATNVGHQVQLQSGPEVLPVSPGVSKISCKSGGTFPFDYAMHWVKOSHAKSLE 65
OY 6 VFELPLSTTVSHQATVYQSGALVRSAGVSKMSKASGYTLTSYMMHWKQTPGGGLE 65
OY 66 WIGVISTNGTSTYNQKFKGATMTVYKSSSTVMEELARLTSEDSANLYCAR-YGYGFPD 124
WIGNIFPENGSTYYNNQKFKGRASLTADTSSSTAYMQLNSLSEDSAYYFCARGWEGCALD 125
OY 125 YWGGGTTLTVSS 136
OY 126 YWGGSTVTVSS 137

RESULT 15
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (REL. 01, CREATED)

```

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (J558).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUHERIA; RODENTIA.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE: 80078170.
 RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
 RL NATURE 283:35-40(1980).
 CC -I- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
 CC THE D AND J SEGMENTS.
 CC -I- THIS PROTEIN BINDS DEXTRAN.
 DR PIR: A26242; MHMS15.
 DR HSP; P01789; 2FGW.
 KW IMMUNOGLOBULIN V REGION.
 FT DISULFID 22 96 BY SIMILARITY.
 FJ NON TER 117 117
 SE SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 52.7%; Score 584; DB 1; Length 117;
 Best Local Similarity 72.4%; Pred. No. 5.05e-108;
 Matches 84; Conservative 13; Mismatches 16; Indels 3; Gaps 2;

Db 4 LQOSGPELVKPGASVKMSCKASGYTFDYMKWKVQSHKSLKLEWIGDINPNNGSTSYNOK 63
 OY 23 LQOSGAELVRSASVKMSCKASGYTLTISNMHWKOTPGGLEWIGNIFPGNGDTYNNOK 82
 Db 64 FKGAATLVDRKSSSTAYMQLNSTSEDSAVYYCARDRYW--YFDVWGAGTYVTYSS 117
 OY 83 FKGRASLTADTSSSTAYMQISLTSEDSAVYFCARGN--WEGALDIWGCGTSYTVSS 137

Search completed: Thu Apr 15 17:59:47 1999
 Job time : 13 secs.


```
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
CC49 FAB PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA ABERGEL C., PADLAN E.A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
RA SCHLOM J.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M95575; G193217; -.
DR PFAM: PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 >134 CC49 FAB.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14957 MW; 7EB07046 CRC32;
Query Match 61.0%; Score 676; DB 11; Length 134;
Best Local Similarity 72.3%; Pred. No. 7,49e-129;
Matches 99; Conservative 18; Mismatches 17; Indels 3; Gaps 2;

Db 1 MEMSWFLFELSVTGVHSQVLOQSDAELVKGASVKISCKASGYTFTHAIHWKOMP 60
OY 1 MEGSWFLFELSVTGVHSQVLOQSDAELVKGASVKISCKASGYTFTHAIHWKOMP 60
Db 61 EGGELMIGFSPGNDPFXKNEFKKATLTADKSSSTAYVQLNLSLSEDSAVYFCTRS- 119
OY 61 GGGELMIGIFPGNDPTYNOKFKKASLTADTSSSTAYVQLNLSLSEDSAVYFCARGNW 120
Db 120 N-MAYWGQSTVTVSS 134
OY 121 EGGALDYGQSTVTVSS 137

RESULT 3
ID 061250 PRELIMINARY; PRT; 152 AA.
AC 061250;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DR ANTIGEN, B-CELL RECEPTOR PRECURSOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C.
RC MEDLINE: 96134009.
RA THIRION S., MOTMANS K., HEYLIEN H., RAUS J., VANDEYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
DR EMBL: L43567; G899071; -.
DR PFAM: PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 152 ANTIGEN, B-CELL RECEPTOR.
SQ SEQUENCE 152 AA; 16517 MW; A83EE9253 CRC32;
Query Match 58.4%; Score 648; DB 11; Length 152;
Best Local Similarity 65.7%; Pred. No. 3,41e-122;
Matches 92; Conservative 24; Mismatches 22; Indels 2; Gaps 2;

Db 6 ILFLVATATGVHSQVLOQSGPELVKPGASVKMSCKASGYTFSSVHMHWKOKAGGLE 65
OY 6 VFLFLSTTGVHSQVLOQSGAELVRSKASGYTLTSSVNMHWKQTPGGLGLE 65
Db 66 WIGYNPNNDVTKYNGKRGKATLTSDKSSSTAYVELSLSEDSAVYFCARGNVDYDG 125
OY 66 WIGNFPNGDITVYNGKRGKASLTADTSSSTAYVQLNLSLSEDSAVYFCARGNW-E-GA 123
Db 126 IAYWGQSTVTVSSGESLQF 145
```

```
OY 124 LDYWGQSTVTVSSAKTTPP 143

RESULT 4
ID P97746 PRELIMINARY; PRT; 120 AA.
AC P97746;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 96366461.
RA KIMURA N., YOSHIKAWA H., IWAMOTO M., SAKIHAMA T., AKASU F., IZUI S.,
RA UENO A., NAKAJIMA Y., TASAKA K.;
RL HYBRIDOMA 14:523-528(1995).
DR EMBL: S82857; G1835936; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 120 AA; 13147 MW; 3EA54DB8 CRC32;
Query Match 56.4%; Score 625; DB 11; Length 120;
Best Local Similarity 75.4%; Pred. No. 9,72e-117;
Matches 89; Conservative 15; Mismatches 11; Indels 3; Gaps 1;

Db 3 LQSGVTLARFGASVKMSCKASGYTFSSVNMHWKORPGGLEWIGATYPGNSDPTVSNOK 62
OY 23 LQSGAELVRSKASVKMSCKASGYTLTSSVNMHWKQTPGGLMIGNIFPGNGDTYNNOK 82
Db 63 FKRAKLTAVTSASTAYVELSLTNEEDSAVYCTRDYDGSAGAFDYWGQSTVTVSS 120
OY 83 FKRAKSLTADTSSSTAYVQLNLSLSEDSAVYFCARGNMGES--ALDYWGQSTVTVSS 137

RESULT 5
ID 009200 PRELIMINARY; PRT; 118 AA.
AC 009200;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
OS UNKNOWN.
OC UNCLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=(NZBXNZ) F1 MOUSE; TISSUE=SPLEEN;
RA PAYELLE-BROGARD B.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U44925; G1763747; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12937 MW; FF570A07 CRC32;
Query Match 55.5%; Score 615; DB 11; Length 118;
Best Local Similarity 75.4%; Pred. No. 2,27e-114;
Matches 89; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Db 1 QVOLLSEGAELARFGASVKMSCKASGYTFSSVNMHWKORPGGLEWIGATYPGNSDPTVSNOK 60
OY 20 QVALLSEGAELVRSKASVKMSCKASGYTLTSSVNMHWKQTPGGLMIGNIFPGNGDTY 79
Db 61 NOKRKRAKTLTADSSSTAYVQLNLSLSEDSAVYFCARGSLGLPDTWGQSTVTVSS 118
OY 80 NOKRKRAKSLTADTSSSTAYVQLNLSLSEDSAVYFCARGNMGALDYWGQSTVTVSS 137

RESULT 6
ID 009199 PRELIMINARY; PRT; 118 AA.
```



```

OS MUS MUSCULUS (MOUSE).
OC EUKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; RODENTIA.
[1]
RP SEQUENCE FROM N.A.
RA KLIMKA A., BARTH S., MATTHEY B., LEMKE H., ARENDIS J.W., DIEHL V.,
RA HOOGENDOORN H., ENGERT A.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF002242; G2290774; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 243 AA; 26225 MW; E0AD5363 CRC32;

Query Match 50.9%; Score 564; DB 11; Length 243;
Best Local Similarity 68.6%; Pred. No. 2,43e-102;
Matches 81; Conservative 17; Mismatches 18; Indels 2; Gaps 1

Db 4 LQSGELAFPGAAYKMSCKASGTYTDDYMMHWKQRPQGLEWIGYINPNATYTDYNOK 63
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 LQSGALVYSGAVSKMSCKASGTYTTSYMMHWKQTPGGGLEWIGINFPNGNDTYNOK 82

Db 64 FKDKATITLAKSSSTAYMQLRLSLSEDSAYVYCAKKTQTQTMGFPFGQGTIVYSSG 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 FKGAASLTADTSSTAYMQLSLTSEDSAYVFCARGWME--LDYWGQGTSTVYSSA 138

RESULT 9 PRELIMINARY; PRT; 123 AA.
ID Q61218;
AC Q61218;
DT 01-NOV-1996 (TREMBL,REL. 01, CREATED)
DT 01-NOV-1996 (TREMBL,REL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBL,REL. 07, LAST ANNOTATION UPDATE)
DE ANTI-DNA HEAVY CHAIN (FRAGMENT).
GN J558.
OS MUS MUSCULUS (MOUSE).
OC EUKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
[1]
RP SEQUENCE FROM N.A.
RA STRAIN-C3H/HEJ-LPR/LPR;
RA WLOCH M.K., ALEXANDER A.L., PIPPEN A.M.M., PISETSKY D.S.,
RA GILKESON G.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U59154; G1389780; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13806 MW; DA290D89 CRC32;

Query Match 48.0%; Score 532; DB 11; Length 123;
Best Local Similarity 65.8%; Pred. No. 7.84e-95;
Matches 79; Conservative 19; Mismatches 17; Indels 5; Gaps 2

Db 4 LQSGELVYPGAIVKISKASGYSTFGYMMNMYKOSHGKSLLEWVGINPYGGTRYOK 63
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 23 LQSGALVYSGAVSKMSCKASGTYTTSYMMHWKQTPGGGLEWIGINFPNGNDTYNOK 82

Db 64 FKDKATITLVKSSSTAYMQLNLTSEDSAYVYCARDYTYTYTDEGCFAYWGQGLTVSA 123
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 83 FKGAASLTADTSSTAYMQLSLTSEDSAYVFCARG---NW-EGALDYWGQGTSTVYSS 137

RESULT 10 PRELIMINARY; PRT; 116 AA.
ID Q35529;
AC Q35529;
DT 01-JAN-1998 (TREMBL,REL. 05, CREATED)
DT 01-JAN-1998 (TREMBL,REL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBL,REL. 07, LAST ANNOTATION UPDATE)
DE ANTI-ACID PHOSPHATASE VARIABLE HEAVY CHAIN 18 (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA TAKATA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,
RA HATANO S.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D50137; D1024480; -.
DR PFAM: PF00047; 19.
FT NON_TER 1
FT NON_TER 116
FT SEQUENCE 116 AA; 13097 MW; BEF6E61A CRC32;
QY
Query Match 46.3%; Score 513; DB 11; Length 116;
Best Local Similarity 66.1%; Pred. No. 2,16e-90;
Matches 76; Conservative 16; Mismatches 21; Indels 2; Gaps 1;

Db 4 LQESGPELVKPGASVEISIKASGYSTFYIYMHMKQSHVKSLEWIGRINPYNQVISTYNN 63
QY 23 LQSGAGELVRGASVKKSCKASGYTLTISYNNHMKQIPGCGLEWIGRINPFGNGDTIYNOK 82
L 64 FKDKASLTVDKSSSTAYWEHLSTLSEDSAYYYCARPT--VDFDYWGQGTIVTSS 116
QY 83 FKGRASLTADSSSTAYWQISLTSEDSAYVFCARGHWEGALDYWGQGTIVTSS 137

RESULT 11 PRELIMINARY; PRT; 120 AA.
ID 035528;
AC 035528;
DT 01-JAN-1998 (TREMBLREL, 05, CREATED)
DT 01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION UPDATE)
DE ANTI-ACID PHOSPHATASE VARIABLE LIGHT CHAIN 11 (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA TAKATA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,
RA HATANO S.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D50136; D1024479; -.
DR PFAM: PF00047; 19.
FT NON_TER 1
FT NON_TER 120
FT SEQUENCE 120 AA; 13235 MW; 9C34DC15 CRC32;
QY
Query Match 46.3%; Score 514; DB 11; Length 120;
Best Local Similarity 65.0%; Pred. No. 1.26e-90;
Matches 76; Conservative 19; Mismatches 20; Indels 2; Gaps 2;

Db 4 LKESGPNLVKPGASVKSICKASGYSTFYIYHWKQSHVKSILKIGRINPYNQATSYNN 63
QY 23 LQSGAGELVRGASVKKSCKASGYTLTISYNNHMKQIPGCGLEWIGRINPFGNGDTIYNOK 82
Db 64 FNDKASLTVDKSSSTAYWEHLSTLSEDSAYYYCAITTVEDYAVDYWGQGTIVTSS 120
QY 83 FKGRASLTADSSSTAYWQISLTSEDSAYVFCARGHW-EG-ALDYWGQGTIVTSS 137

RESULT 12 PRELIMINARY; PRT; 249 AA.
ID P97512;
AC P97512;
DT 01-MAY-1997 (TREMBLREL, 03, CREATED)
DT 01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE)
DE SINGLE CHAIN FV ANTIBODY (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA ARTSARENKO O., WELTER E.W., MUENTZ K., CONRAD U.;

```

```

RL J. PLANT PHYSIOL. 144:427-429(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96086099.
RA ARTSANKO O., PEISER M., ZUR NIEDEN U., FIEDLER U., WEILER E.W.,
RA MUMENTZ K., CONRAD U.;
RL PLANT J. 8:745-750(1995).
DR EMBL; Z29480; E283450; -.
FRAM; PF00047; 19.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 249 AA; 249 26939 MW; 428B904E CRC32;

Query Match 46.3%; Score 514; DB 11; Length 249;
Best Local Similarity 62.2%; Pred. No. 1,26e-90;
Matches 74; Conservative 18; Mismatches 26; Indels 1; Gaps 1

Db 1 OVQLOQSGAEIYVRGASVYKLSCTASGFENKXDYIHWVKQREKLEWIGRIAPASGVKY 60
OY 20 QAVIQQSSAEIYVRGASVYKMSCKASGTLTYSNMHWKQPGGLEWIGRIAPGNGDTYY 79
Db 61 VPRFDKATITADTSNTAYLLLSLSESDYAVYYCARBDITLYSLGWGCGTIVTVSS 119
OY 80 NQKFKGRASLTADSSSTAYVWQISLSLSESDAVYFCAR-GWMEGALDYYWGCGTIVTVSS 137

RESULT 13
ID 055113; PRELIMINARY; PRT; 98 AA.
AC 055113;
DT 01-JUN-1998 (TREMBL,REL. 06, CREATED)
DT 01-JUN-1998 (TREMBL,REL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBL,REL. 06, LAST ANNOTATION UPDATE)
DE A6 ANTI-[4-HYDROXY-3-NITROPHENYL(PHENOLATE FORM)] ACETYL MAB V-H
DE REGION (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88198051.
RA SOBRANDRIO A., AZUMA T., HAMADA Y., SAKATO N., FUJIO H.;
RL J. BIOCHEM. 102:1337-1343(1987).
DR EMBL; D00233; D1019624; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 98 AA; 10865 MW; 4C615AE9 CRC32;

Query Match 46.2%; Score 512; DB 11; Length 98;
Best Local Similarity 74.2%; Pred. No. 3.70e-90;
Matches 72; Conservative 12; Mismatches 13; Indels 0; Gaps 0

Db 1 OVQLOQSGAEIYVRGASVYKLSCTASGFENKXDYIHWVKQREKLEWIGRIAPASGVKY 60
OY 20 QAVIQQSSAEIYVRGASVYKMSCKASGTLTYSNMHWKQPGGLEWIGRIAPGNGDTYY 79
Db 61 NEKFKRATITVDRPSSTAYVWQISLSLSESDAVYVCA 97
OY 80 NQKFKGRASLTADSSSTAYVWQISLSLSESDAVYFCA 116

RESULT 14
ID 099846; PRELIMINARY; PRT; 125 AA.
AC 099846;
DT 01-MAY-1997 (TREMBL,REL. 03, CREATED)
DT 01-MAY-1997 (TREMBL,REL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBL,REL. 06, LAST ANNOTATION UPDATE)
DE PLATELET MEMBRANE GLYCOPROTEIN IB (GP1B) SPECIFIC ANTIBODY (FRAGMENT).
DE V1-02.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]

```


THIS PAGE BLANK (USPTO)